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<p>(54) Title: SCREENING METHOD FOR MENA PROTEIN INVOLVED IN MICROFILAMENT DYNAMICS</p> <p>(57) Abstract</p> <p>Two novel mammalian genes <i>Mammalian Ena (Mena)</i>, and <i>Ena-VASP like (Evl)</i> encoding novel proteins Mena, and Evl are disclosed. Mena and Evl proteins have a discrete, EVH1 functional domain responsible for Mena binding to ActA of <i>Listeria</i>, and to the cytoskeletal proteins zyxin and vinculin. The EVH1 domain of Mena is also responsible and sufficient for targeting localization of Mena and Mena based fusion proteins to focal adhesions, and to the surface of <i>Listeria</i> cells at the polar site of induction of actin comet tail formation. Based on the Mena and Evl genes and proteins disclosed herein, a variety methods and compositions are provided for screening, isolating, and characterizing endogenous and exogenous factors, drugs and therapeutic agents useful to evaluate and/or control cytoskeletal dynamic events involved in normal and abnormal cell morphology, adhesion, motility, growth and/or differentiation.</p>		

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## SCREENING METHOD FOR MENA PROTEIN INVOLVED IN MICROFILAMENT DYNAMICS

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**Technical field:**

The invention relates to DNA sequences encoding proteins involved in microfilament dynamics. More specifically, the invention relates to DNA sequences and proteins involved in microfilament dynamics affecting normal and abnormal cell morphology, adhesion, motility, growth and differentiation, as well as pathogenicity of certain viruses and bacteria, and to screening, diagnostic and therapeutic methods and compositions employing these DNA sequences and proteins.

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**BACKGROUND OF THE INVENTION**

The control of cell morphology, motility, growth and differentiation generally requires coupling of external stimuli to processes that regulate cytoskeletal architecture. The mechanical forces that drive morphological change and migration arise initially from the microfilament-based cytoskeleton (reviewed by Lauffenburger and Horwitz, Cell 84: 359-369, 1996; Mitchison and Cramer, Cell 84: 371-379, 1996). In particular, formation of cellular protrusions such as filopodia and lamellipodia requires polymerization and stabilization of F-actin. A growing body of evidence links various signal transduction pathways to the regulation of these cytoskeletal processes (reviewed by Zigmond, Current Opinion in Cell Biology 8: 66-73, 1996), but the final integration of these signals with regulation of *de novo* actin polymerization is a complicated process that remains to be elucidated.

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Actin-driven formation of membrane protrusions is the first step in migration of neuronal growth cones (Forscher et al., Nature 357: 515-8, 1992; Forscher and Smith, S.,

J. Cell Biol. **107**: 1505-1516, 1988; Sanders and Wang, J. Cell Sci. **100**., 771-780, 1991).

Establishment of proper connections in the central nervous system depends on the ability of neuronal growth cones to guide neurites to their final targets. Genetic analyses have been used to probe the relationship between signal transduction pathways and neuronal development.

One signaling pathway implicated in the processes of axonal outgrowth in neural development is mediated by the *Drosophila* homolog of the c-Abl tyrosine kinase (Gertler, Thesis, University of Wisconsin-Madison, 1992; Gertler et al., Cell **58**: 103-113, 1989; Gertler et al., Science **248**: 857-60, 1990; Gertler et al., Genes Dev. **7**: 441-453, 1993; Henkemeyer et al., Cell **63**: 949-960, 1990). Simple *Abl* mutant animals survive past metamorphosis. However, *Abl* mutants that are also heterozygous for a mutation in *Disabled* (*Dab*), or one of 4 other loci identified in genetic modifier screens, require Abl tyrosine kinase activity for post-pupal viability and proper formation of the embryonic central nervous system (CNS). Animals that are homozygous mutant for both *Abl* and *Dab* make few or no proper axonal connections.

The defects caused by loss of Abl, Dab or both are ameliorated by mutations in the *Drosophila Enabled* (*Ena*) gene (Gertler et al., Genes Dev. **9**: 521-33, 1995; Gertler et al., Science **248**: 857-60, 1990). *Ena* was the only locus recovered in repeated genetic screens for dose-dependent suppressors of *Abl*- and *Dab*- dependent phenotypes. In the homozygous state, *Ena* mutations cause a recessive lethal phenotype that includes defects in the embryonic CNS. Ena protein is concentrated in CNS axons, like Abl and Dab, and has a proline-rich core which binds *in vitro* to the SH3 domains of Abl and Src, but not to the SH3 domains of several other proteins tested (Gertler et al., Genes Dev. **9**: 521-33, 1995). Ena is tyrosine phosphorylated *in vivo*. The phosphotyrosine content of Ena is reduced approximately three-fold in *Abl* mutant pupae, indicating that Ena is phosphorylated by Abl-dependent and independent tyrosine kinases. Over expression and *in vitro* phosphorylation studies demonstrate that Abl can phosphorylate Ena directly. However, Abl-mediated phosphorylation of Ena is not absolutely required for axonogenesis, as the need for Abl tyrosine kinase activity in this process is exposed only in combination with mutations in sensitizing loci such as *Dab* (Henkemeyer et al., Cell **63**: 949-960, 1990).

While the above findings implicate Ena as an important factor in Abl mediated regulation of axonal development, more specific knowledge is required to fully elucidate the

function and regulation of Ena in axonogenesis and cytoskeletal dynamics in *Drosophila* and other organisms.

In addition to the neural development model of Abl-mediated cytoskeletal regulation, a second model for studying microfilament assembly and function has been developed based on certain intracellular bacteria that recruit host cytoskeletal proteins to achieve bacterial motility. The cytoskeletal dynamics involved in intracellular movement of these bacteria bears some resemblance to the actin dynamics in lamellipodia of motile eukaryotic cells (Theriot et al., Trends Cell Biol. 2: 219-222, 1992), suggesting that that these model systems may be useful for determining the molecular bases of actin-based cell motility. The most widely studied motile bacteria in this context is *Listeria monocytogenes*, an ubiquitous Gram-positive bacterium responsible for severe, food born infections in humans and animals. *Listeria* motility and intercellular infection depends on the asymmetric recruitment of host profilin, an actin monomer binding protein, to one pole of the bacteria where rapid polymerization of actin is induced to form a microfilamentous "comet tail" that drives bacterial movement (Theriot et al., Cell 76: 505-517, 1994).

The interaction of profilin with the surface of *Listeria* is indirect and requires a bacterial gene *actA* (Chakraborty et al., EMBO J. 14: 1314-1321, 1995). The product of the *actA* gene is a surface bound polypeptide, and is the sole bacterial factor needed for the inducement of host actin polymerization (Id.). However, recent findings have shown that *Listeria* grown in culture does not associate efficiently with either actin (Tilney and Tilney, Trends Microbiol. 1: 25-31, 1993) or profilin (Theriot et al., Cell 76: 505-517, 1994, suggesting that recruitment of these proteins also requires a host cytoplasmic factor.

Recent observations implicate the Vasodilator-Stimulated Phosphoprotein (VASP) as a candidate factor involved in ordinary cytoskeletal dynamics, and as a host factor in the regulation of *Listeria* induced microfilament assembly. Specifically, the VASP protein is an abundant *in vivo* substrate for cyclic-nucleotide dependent kinases (Halbrügge et al., J. Biol. Chem. 265: 3088-3093, 1990; Halbrügge and Walter, J. Chromatogr. 521: 335-343, 1990; Halbrügge and Walter, Eur. J. Biochem. 185: 41-50, 1989; Waldmann et al., Eur. J. Biochem. 167: 441-448, 1987). VASP is distributed along microfilaments, is particularly concentrated at sites of focal contact and in the peripheral lamellae of spreading or migrating cells, and there is evidence of direct contact between VASP and F-actin (Reinhard et al., EMBO J. 11: 2063-2070, 1992; Haffner et al., EMBO J. 14: 19-27, 1995). VASP also

contains a central region of proline-rich sequences comprising a proposed binding domain for the actin binding protein profilin (Reinhard et al., EMBO J. 14: 1583-1589, 1995). In *Listeria* infected cells, VASP is recruited to the bacterial surface by direct binding with the ActA surface protein (Chakraborty et al., EMBO J. 14: 1314-1321, 1995; Pistor et al., Curr. Biol. 5: 517-525, 1995). VASP accumulates on the bacterial surface prior to the formation of F-actin clouds that precede comet tail formation, and is later localized at the site of actin filament assembly between the polar bacterial surface and the front of the actin tail (Chakraborty et al., EMBO J. 14: 1314-1321, 1995). VASP is also a ligand for profilin (Reinhard et al., EMBO J. 14: 1583-1589, 1995). These findings suggest a role for VASP in ordinary cytoskeletal dynamics, and as a host factor required for *Listeria* motility.

Although the recent discovery and preliminary characterization of Ena and VASP lends basic insight into cytoskeletal dynamics and bacterial motility, many questions remain concerning the specific mechanisms and regulation of these processes. Accordingly, there is a general need in the art for further discovery and characterization of structural and regulatory factors involved in microfilament dynamics affecting normal and abnormal cell morphology, adhesion, motility, growth and differentiation. Likewise, there remains a general need for additional discovery and characterization of factors involved in pathogenicity and motility of bacteria and other pathogens which rely on the induction of host cytoskeletal processes for transmission and virulence. Until these fundamental needs are satisfied, there will also remain more specific needs in the art for effective tools to model, diagnose and treat defects in cytoskeletal structure and regulation attributable to such diverse conditions as cancer, traumatic neural injury and cytopathologic bacterial infection.

### SUMMARY OF THE INVENTION

It is therefore an object of the present invention to identify and characterize factors involved in microfilament dynamics affecting normal and abnormal cell morphology, adhesion, motility, growth and differentiation.

It is a further object of the invention to identify and characterize factors involved in microfilament dynamics affecting pathogenicity and motility of bacteria and other pathogens which rely on the induction of host cytoskeletal processes for transmission and virulence.

It is yet another object of the invention to provide tools to more effectively model, diagnose and treat defects in cytoskeletal structure and regulation attributable to injury and disease.

The invention achieves these objects and other objects and advantages which will become apparent from the description which follows by providing two novel mammalian genes *Mammalian Ena (Mena)*, and *Ena-VASP like (Evl)* encoding novel proteins Mena, and Evl. The Mena and Evl proteins provided herein possess novel biochemical and cell biological properties rendering these proteins useful in the study and/or control of a variety of microfilament dynamic processes. In addition, the Mena and Evl proteins disclosed herein are useful for generating, isolating, and characterizing additional endogenous and exogenous factors, drugs and other agents useful for evaluating and/or controlling cytoskeletal dynamics involved in normal and abnormal cell morphology, adhesion, motility, growth and/or differentiation. Reflective of these uses, the invention provides several methods and tools specifically directed to the diagnosis and treatment of injury and disease conditions involving cytoskeletal dynamic processes, such as metastatic cancer and infection by cytopathogenic bacteria.

Within one aspect of the invention, purified and isolated polynucleotides are provided which encode a native Mena or Evl protein. Among these polynucleotides are DNA sequences encoding specific native isoforms of Mena, including an approximately 140 kD, neural-specific isoform of Mena, an approximately 60 kD hematopoietic-specific Mena isoform, and approximately 80 kD and 88 kD isoforms of Mena which are broadly distributed among different mammalian tissue types.

In related embodiments of the invention, *Mena* or *Evl* based polynucleotides are provided that encode Mena or Evl proteins or fragments thereof, recombinantly produced peptide derivatives, fusion proteins and the like incorporating only a portion of Mena or Evl, and up to the entire Mena or Evl protein. Among these *Mena* or *Evl* based polynucleotides are sequences that encode discrete functional domains of the Mena or Evl protein responsible for specific biological activities of the intact protein. Preferred functional domains in this context include an N-terminal domain of Mena and Evl that mediates binding of Mena to certain proline-rich ligands, including ActA, zyxin and vinculin, and which directs localization of Mena and heterologous proteins linked to the EVH1 domain to focal contacts, and to the surface of cytopathogenic bacteria. Also provided are mutagenized

polynucleotides that encode mutant analogs of the Mena or Evl protein, or of selected polypeptide portions of Mena or Evl such as the EVH1 functional domain, which exhibit modified biological activity compared to native Mena or Evl proteins and polypeptide domains.

5           Within another aspect of the invention, substantially pure Mena or Evl proteins are provided, including a variety of tissue specific or broadly distributed Mena and Evl isoforms disclosed herein. Also provided are Mena or Evl based synthetic peptides or fragments thereof, recombinantly produced peptides, fusion proteins and the like incorporating all or a portion of Mena or Evl, including peptides corresponding to the aforementioned Mena or  
10       Evl functional domains, as well as mutant analogs of the Mena or Evl protein or polypeptide portions thereof.

          Within a related aspect of the invention, antibodies, antibody derivatives and chimeric antibodies are provided that bind to one or more of the Mena and Evl proteins and isoforms thereof. Also provided are antibodies, antibody derivatives and chimeric antibodies that bind  
15       to one or more of the Mena or Evl based synthetic peptides, recombinantly produced peptides, fusion proteins and the like disclosed herein.

          Within yet another aspect of the invention, *Mena* or *Evl* based recombinant polynucleotide expression constructs are provided which include a polynucleotide insert encoding a Mena or Evl protein or Mena or Evl based synthetic peptide, recombinantly  
20       derived peptide, fusion protein or the like operably incorporated within an expression vector capable of directing expression of the polynucleotide insert sequence in a mammalian host cell. Various such constructs are provided, including constructs that incorporate polynucleotide sequences encoding the native 140 kD, 60 kD, 80 kD or 88 kD Mena isoforms. Also provided are related constructs that incorporate polynucleotide  
25       insert sequences encoding Mena or Evl proteins or fragments thereof, recombinantly derived peptides, fusion proteins and the like including native or mutagenized forms of the Mena or Evl protein or of selected polypeptide portions of Mena or Evl such as the EVH1 functional domain.

          Within related aspects of the invention, *Mena* or *Evl* based expression constructs  
30       are employed in methods for modulating expression of *Mena* or *Evl*, disrupting *Mena* or *Evl* expression or inducing ectopic expression of *Mena* or *Evl* genes and related polynucleotide sequences in mammalian host cells. The expression constructs are



introduced into the host cells by microinjection, transfection or other suitable method to achieve transformation of the host cell, and the host cell is cultured, transplanted or left *in situ* under suitable conditions to allow the host cell to express the *Mena* or *Evl* based polynucleotide insert sequence.

5           Within additional aspects of the invention, a variety of screening and diagnostic methods and compositions are provided that employ one or more of the aforementioned inventive tools. For example, the invention provides screening, diagnostic and therapeutic methods that utilize *Mena* or *Evl* encoding polynucleotides, *Mena* or *Evl* proteins, peptides, fusion proteins and the like, *Mena* or *Evl* binding antibodies, *Mena* or *Evl* based expression  
10 constructs, and/or mammalian host cells transformed to express *Mena* or *Evl* insert sequences.

          In preferred screening and diagnostic methods of the invention, labeled *Mena* or *Evl* proteins and peptides, as well as anti-*Mena* or anti-*Evl* antibodies, are used to determine the localization and activity of *Mena* or *Evl* in normal and abnormal cytoskeletal dynamic  
15 processes. In one such method, labeled *Mena* proteins, peptides and antibodies are introduced into the cytoplasm of *Listeria* infected cells to detect and quantify recruitment of *Mena* to the bacterial surface at the polar site of comet tail formation, and to detect and quantify the activity of *Mena* in mediating *Listeria* induction of microfilament polymerization. In more specific methods, labeled *Mena* and anti-*Mena* antibodies are used  
20 to detect and quantify *Mena* binding to ActA, profilin, zyxin or vinculin. Each of these methods in turn provide a basis for additional methods to screen for agonists and antagonists of specific *Mena* activities involved in the *Listeria* microfilament induction pathway.

          In related screening and diagnostic methods, *Mena* or *Evl* proteins and peptides, as well as anti-*Mena* or anti-*Evl* antibodies, are used to detect and quantify *Mena* or *Evl*  
25 activity in normal and abnormal cytoskeletal dynamic processes under endogenous control. As in the *Listeria* microfilament induction model, localization and quantification of *Mena* or *Evl* associated with dynamic cytoskeletal structures or events, or with specific molecular factors involved in cytoskeletal regulation, provides the basis for a variety of methods to diagnose abnormal cytoskeletal processes associated with disease, and to screen for agonists  
30 and antagonists of specific *Mena* activities involved in such processes. In one example, labeled *Mena* protein is used as a reagent to screen small molecule and peptide libraries to identify inhibitors of *Mena* activity. In more specific examples, an overlapping set of

chemically synthesized peptides is generated covering the sequence of a selected Mena ligand, such as ActA, Profilin or Zyxin, and this library is screened using covalently or antibody labeled Mena to identify highly specific and potent peptide inhibitors.

In other related screening and diagnostic methods, Mena or Evl based synthetic peptides, recombinantly produced peptides, fusion proteins and the like incorporating all or a portion of Mena or Evl, as well as mutant analogs of Mena or Evl proteins or peptides, are used to screen for specific agonists and antagonists of Mena or Evl activities. In one such method, the EVH1 domain of Mena or Evl, or an EVH1 consensus peptide having a conserved amino acid sequence between Mena, Evl and VASP, is used as an affinity reagent to identify as yet unknown cellular factors involved in cytoskeletal regulation, or as a labeled probe to screen cDNA expression libraries to identify genes encoding such unknown regulatory factors.

Other screening and diagnostic methods of the invention rely on labeled polynucleotide probes to map the chromosomal locations of Mena, Evl and related genes, to identify genetic defects in these genes among cell populations or individuals, and to detect and measure expression of Mena, Evl or related genes in association with specific cytoskeletal dynamic structures, events or molecular regulatory factors.

In addition to screening and diagnostic methods, the invention provides a range of therapeutic methods for preventing and/or treating diseases and other conditions that involve aberrant cytoskeletal regulation, for example pathogenic infection, traumatic neural injury and cancer. Therapeutic methods of the invention variously utilize Mena or Evl encoding polynucleotides, Mena or Evl proteins and peptides, Mena or Evl binding antibodies, *Mena* or *Evl* based expression constructs, mammalian host cells transformed to express *Mena* or *Evl* insert sequences, and other therapeutic agents such as triplex forming oligonucleotides, antisense polynucleotides or ribozymes that specifically target *Mena* and/or *Evl* polynucleotides.

In preferred therapeutic methods directed to the treatment of pathogenic infection and cancer, it is useful to employ agents that inhibit Mena or Evl expression or activity and thereby eliminate or impair aberrant recruitment of Mena by pathogens, or interrupt Mena expression or activity associated with cancerous cell migration. Useful inhibitors in this context include antibodies that block or impair Mena or Evl by binding to the protein, Mena or Evl based, synthetic or recombinantly produced peptides, fusion proteins that

compete for Mena or Evl binding partners or otherwise block or impair Mena or Evl expression or activity, triplex forming oligonucleotides, antisense polynucleotides or ribozymes that block expression of *Mena* and/or *Evl* polynucleotides, and mutant *Mena* or *Evl* based expression constructs that abolish or reduce Mena or Evl expression or activity  
5 in targeted cells.

In preferred therapeutic methods directed to the treatment of traumatic neural injury and other injury conditions where it is desirable to promote cell migration for neural regeneration or wound healing, it is useful to employ agents that induce or enhance Mena or Evl expression or activity. Useful agents in this context include anti-Evl antibodies,  
10 Mena or Evl based, synthetic or recombinantly produced peptides, fusion proteins and the like that enhance Mena or Evl binding to its partners or otherwise enhance Mena or Evl expression or activity, and mutant *Mena* or *Evl* based expression constructs that induce or enhance Mena or Evl expression or activity in targeted cells.

## 15 DETAILED DESCRIPTION OF THE INVENTION

The present invention provides two novel mammalian genes *Mammalian Ena* (*Mena*), and *Ena-VASP like* (*Evl*) which encode novel proteins Mena, and Evl. Sequences encoding Mena and Evl include those sequences that result in minor variations in amino acid sequence, such as those due to genetic polymorphisms, allelic variations, differences between  
20 species and those in which blocks of amino acids have been added, altered or replaced without substantially altering the biological activity of the proteins. The *Mena* and *Evl* genes and Mena and Evl proteins disclosed herein are useful for generating, isolating, and characterizing endogenous and exogenous factors, drugs and other agents that can be employed in methods to evaluate and/or regulate cytoskeletal dynamic processes involved in  
25 normal and abnormal cell morphology, adhesion, motility, growth and/or differentiation. Within these general methods the invention provides specific methods directed toward the diagnosis and treatment of injury and disease conditions involving cytoskeletal dynamic processes, such as metastatic cancer and infection by cytopathogenic bacteria.

Within one aspect of the invention, purified and isolated polynucleotides are  
30 provided which encode a native Mena or Evl protein. Among these polynucleotides are DNA sequences encoding specific isoforms of native Mena or Evl. Preferred methods to isolate and purify polynucleotides encoding native Mena or Evl employ conventional

screening, subcloning and polymerase chain reactions, for example according to the methods and using the reagents described in Sambrook et al., (1989) *Molecular Cloning A Laboratory Manual* (Cold Spring Harbor, NY: Cold Spring Harbor Press). In one example, a restriction fragment of the *Drosophila* gene *Ena* (Gertler et al., Genes Dev. 9: 521-533, 1995, which is incorporated herein by reference in its entirety) is used to probe a mammalian cDNA library made from mouse embryonic stem cells (Chen et al., Genes Dev. 8: 2293-2301, 1994, which is incorporated herein by reference in its entirety). Hybridization of the probe under stringent conditions is detected to identify positive phage candidates for incorporation of a Mena or Evl polynucleotide. Briefly, the positive phage are then purified and their cDNA inserts are subcloned and sequenced. Additional polynucleotide probes that are useful within the invention include Mena or Evl probes corresponding to partial or complete nucleotide sequences generated from the cDNAs depicted in SEQ ID NOS: 1, 3 or 7 below. Degenerate oligonucleotides based on the amino acid sequences of SEQ ID NOS: 2, 4, 5, 6, 8 and 9 are also useful in methods for identifying additional isoforms and related sequences. Alternately, as set forth in more detail below, proteins, synthetic peptides, recombinantly produced peptides, fusion proteins and the like that bind or otherwise interact with Mena can be used as labeled probes to screen mammalian cDNA expression libraries to identify additional genes or cDNAs encoding Mena or Evl proteins. In one such embodiment, known Mena binding partners including ActA, zyxin, vinculin and VASP, are used as probes to detect Mena encoding polynucleotides, for example using well known autoradiographic or immunoassay screening methods.

The choice of hybridization conditions will be evident to one skilled in the art and will generally be guided by the purpose of the hybridization, the type of hybridization (DNA-DNA or DNA-RNA), and the level of relatedness between the sequences. Methods for hybridization are well established in the literature; See, for example: Sambrook, *ibid.*; Hames and Higgins, eds, *Nucleic Acid Hybridization A Practical Approach*, IRL Press, Washington DC, 1985; Berger and Kimmel, eds, Methods in Enzymology, Vol. 52, Guide to Molecular Cloning Techniques, Academic Press Inc., New York, NY, 1987; and Bothwell, Yancopoulos and Alt, eds, Methods for Cloning and Analysis of Eukaryotic Genes, Jones and Bartlett Publishers, Boston, MA 1990; which are incorporated by reference herein in their entirety. One of ordinary skill in the art realizes that the stability of nucleic acid duplexes will decrease with an increased number and location of mismatched bases; thus, the

stringency of hybridization may be used to maximize or minimize the stability of such duplexes. Hybridization stringency can be altered by: adjusting the temperature of hybridization; adjusting the percentage of helix-destabilizing agents, such as formamide, in the hybridization mix; and adjusting the temperature and salt concentration of the wash solutions. In general, the stringency of hybridization is adjusted during the post-hybridization washes by varying the salt concentration and/or the temperature. Stringency of hybridization may be reduced by reducing the percentage of formamide in the hybridization solution or by decreasing the temperature of the wash solution. High stringency conditions may involve high temperature hybridization (e.g., 65–68°C in aqueous solution containing 4–6XSSC, or 42°C in 50% formamide) combined with high temperature (e.g., 5–25°C below the  $T_m$ ) and a low salt concentration (e.g., 0.1X SSC). Reduced stringency conditions may involve lower hybridization temperatures (e.g., 35–42°C in 20–50% formamide) with intermediate temperature (e.g., 40–60°C) and washes in a higher salt concentration (e.g., 2–6X SSC). Moderate stringency conditions, which may involve hybridization at a temperature between 50°C and 55°C and washes in 0.1x SSC, 0.1% SDS at between 50°C and 55°C, may be used to identify clones encoding polynucleotide molecules encoding Mena or Evl from other species or to isolate isoforms of Mena or Evl.

Mena or Ena encoding polynucleotides that are particularly useful within the invention encode Mena or Ena proteins having unique structural and/or biochemical properties, or which exhibit discrete expression or tissue distribution patterns among a various Mena or Ena isoforms. Within the specific examples identified, SEQ ID NO: 1 depicts a Mena cDNA polynucleotide and is deduced amino acid sequence (SEQ ID NOS: 1 and 2) evidently expressed in two isoforms, approximately 80 kD, and 88 kD in size, and exhibiting a broad pattern of tissue distribution in neurons, fibroblasts, kidney epithelium, muscle, neural crest and hematopoietic cells. Other examples identify "*Neural Mena*" cDNA polynucleotides that contain combinations of three alternately included exons and encoding multiple isoforms of Mena (Neural Mena<sup>+</sup>, SEQ ID NO: 4; Neural Mena<sup>++</sup>, SEQ ID NO: 5; and Neural Mena<sup>+++</sup>, SEQ ID NO: 6). In a representative example, a cDNA encoding Neural Mena<sup>+</sup> is disclosed (SEQ ID NO: 3) Unlike Mena, Neural Mena isoforms are approximately 140 kD in size and exhibit neural tissue specific distribution. In yet other examples, cDNA polynucleotides encoding an approximately 60 kD, hematopoietic specific

form of Mena, and cDNA polynucleotides (SEQ ID NOS: 7) encoding the Evl protein (SEQ ID NO: 8) are described.

To evaluate size and distribution of Mena or Evl proteins encoded by different polynucleotides, a variety of well known methods can be used. For example, molecular size of proteins translated from Mena or Ena coding cDNAs *in vitro* can be determined by gel electrophoresis, and tissue distribution can be determined by comparative Western blotting of cell lysates from different tissues, or *in situ* hybridization of whole embryos or tissue sections, using anti-Mena or anti-Evl antibodies (for example according to the general methods disclosed in Harlow and Lane, (1988) Antibodies A Laboratory Manual (Cold Spring Harbor, NY: Cold Spring Harbor Press), which is incorporated herein by reference in its entirety). Other methods of determining the tissue specificity of Mena or Ena encoding polynucleotides include assays that measure Mena or Ena expression between tissue differentiation stages, for example in *in vivo* developmental models or systems where tissue differentiation can be induced by exogenous stimuli. In one such example disclosed herein, Mena protein is assayed by direct anti-Mena immunofluorescence assay in developing embryos and in differentiated P19 embryonic carcinomal cells, to demonstrate that expression of the 140 kD neural specific Mena isoform increases during development at the time of rapid neurite outgrowth, and that subcellular distribution of Neural Mena in P19 cells is concentrated in the growth cones of developing neurites. In a related assay, anti-Mena Western blots of lysates from P19 embryonic carcinomal cells following retinoic acid induction of the cells to differentiate neurofilament-positive neurons (Rudnicki and McBurney, (1987) In Teratocarcinomas and Embryonic Stem Cells: A Practical Approach, E. Robertson, ed., (Oxford, England: IRL Press Limited), pp. 19-47; which is incorporated herein by reference in its entirety) demonstrated that the 140 kD Neural Mena isoform is induced during the neural differentiation process.

Also of particular use within the invention are *Mena* or *Evl* based polynucleotides that encode Mena or Evl proteins or fragments thereof, recombinantly produced peptide derivatives, fusion proteins and the like incorporating only a portion of Mena or Evl, and up to the entire Mena or Evl protein. Among these *Mena* or *Evl* based polynucleotides are sequences that encode discrete functional domains of the Mena or Evl protein responsible for specific biological activities of the intact protein. Functional domains which are of particular interest in this context will be directly involved in structural or regulatory

interactions mediating cytoskeletal dynamic processes, for example localization of Mena or Evl to structures involved in cytoskeletal dynamic processes, or functional association of Mena or Evl with molecular factors that mediate or regulate cytoskeletal dynamic processes. In one example, an N-terminal domain of Mena (N-Mena) including approximately the first  
5 170 amino acids of the protein is demonstrated to mediate binding of Mena to certain proline-rich ligands, including ActA, zyxin and vinculin, and to direct localization of Mena and heterologous proteins linked to the N-Mena peptide to focal contacts, and to the surface of cytopathogenic bacteria. The N-Mena peptide corresponds to a functional domain (the EVH1 domain) that is highly conserved between Mena, Evl and VASP, as demonstrated by  
10 sequence alignment comparisons. A consensus sequence for the alignment is shown in SEQ ID NO. 9.

Within a closely related aspect of the invention, substantially pure Mena or Evl proteins and peptides are provided that are initially encoded by the aforementioned polynucleotides. The Mena and Evl proteins include a variety of tissue specific or broadly  
15 distributed Mena and Evl isoforms disclosed herein. Also provided are Mena or Evl based synthetic peptides, recombinantly produced peptides, fusion proteins and the like incorporating all or a portion of Mena or Evl, including peptides corresponding to the aforementioned Mena or Evl functional domains, as well as mutant analogs of the Mena or Evl protein or polypeptide portions thereof. The proteins or polypeptide portions thereof  
20 may or may not have the biological activity of corresponding native Mena or Evl. Within one example, proteins are prepared that are capable of binding to the proline-rich binding partner ActA, but not capable of inducing profilin.

The peptides can be prepared via chemical synthesis, as described hereinbelow, or by recombinant DNA technology, or as fusion proteins, and the like. Desirably, the peptide will  
25 be as small as possible while still maintaining substantially all of the reactivity of a larger peptide. The subject peptides have an amino acid sequence encoded by a nucleic acid which hybridizes under stringent conditions with an oligonucleotide of 15 or more contiguous nucleotides of SEQ ID NOS: 1,3, or 7. Exemplary amino acid sequences among the subject peptides are shown in SEQ ID NO: 2 (amino acids 6-170 (N-Mena); amino acids 440-537  
30 (C-Mena) and SEQ ID NO: 11. It will be understood that the peptides of the present invention or analogs thereof which have Mena or Evl activity may be modified from a native Mena or Evl sequence as necessary to provide other desired attributes, e.g., improved

binding or inhibitory activity (e.g., increased competition with native protein), improved adsorption to a solid phase, etc. For instance, the peptides may be subject to various changes, such as insertions, deletions, and substitutions, either conservative or non-conservative, where such changes might provide for certain advantages in their use. By

5 conservative substitutions is meant replacing an amino acid residue with another which is biologically and/or chemically similar, e.g., one hydrophobic residue for another, or one polar residue for another. The substitutions include combinations such as Gly, Ala, Val, Ile, Leu; Asp, Glu; Asn, Gln; Ser, Thr; Lys, Arg; and Phe, Tyr. Usually, the sequence of the peptide will not differ by more than about 20% from the native Mena or Evl sequence,

10 except where additional amino acids may be added at either terminus for the purpose of modifying the physical or chemical properties of the peptide for, e.g., ease of linking or coupling, and the like. Having identified different peptides of the invention, in some instances it may be desirable to join two or more peptides in a composition or admixture. The peptides in the composition can be identical or different, and together they should

15 provide equivalent or greater reactivity than the parent peptide(s). The subject peptides find a variety of uses including preparation of specific antibodies. Because of their relatively short size, the peptides can be synthesized in solution or on a solid support in accordance with conventional techniques. Various automatic synthesizers are commercially available and can be used in accordance with known protocols. See, for example, Stewart and

20 Young, Solid Phase Peptide Synthesis, 2d. ed., Pierce Chemical Co. (1984); Tam et al., J. Am. Chem. Soc. 105:6442 (1983); Merrifield, Science 232:341-347 (1986); and Barany and Merrifield, The Peptides, Gross and Meienhofer, eds., Academic Press, New York, pp. 1-284 (1979), each of which is incorporated herein by reference. Short peptide sequences, or libraries of overlapping peptides, usually from about 6 up to about 35 to 50 amino acids,

25 which correspond to the selected regions described herein, can be readily synthesized and then screened in screening assays designed to identify reactive peptides. Alternatively, recombinant DNA technology may be employed wherein a nucleotide sequence which encodes a peptide of the invention is inserted into an expression vector, transformed or transfected into an appropriate host cell and cultivated under conditions suitable for

30 expression. These procedures are generally known in the art, as described generally in Sambrook et al., Molecular Cloning. A Laboratory Manual, Cold Spring Harbor Press, Cold



Spring Harbor, New York (1989); Ausubel et al., (ed.) Current Protocols in Molecular Biology, John Wiley and Sons, Inc., New York (1987), and U.S. Pat. Nos. 4,237,224, 4,273,875, 4,431,739, 4,363,877 and 4,428,941, for example, whose disclosures are incorporated herein by reference.

5           The various biological activities of EVH1 and other functional domains of Mena or Evl can be detected and quantified using a variety of methods, including for example ligand binding assays using immobilized Mena or Evl proteins or fusion proteins. In one such method, PCR is used to generate polynucleotide fragments encoding amino acids corresponding to a selected or putative functional domain, for example amino acids 6-170  
10   representing N-Mena, or amino acids 440-537 representing a C-terminal functional domain of Mena (C-Mena). The polynucleotide fragments are then cloned into a suitable expression vector, for example pGex2T, and fusion proteins are prepared (Smith and Johnson, Gene 67: 31-40, 1988, which is incorporated herein by reference in its entirety). The fusion proteins can be endogenously labeled, for example using a covalent radiolabel or other conventional  
15   marker, or alternately labeled using antibodies that bind to the fusion protein. In one ligand binding example disclosed herein, an N-Mena-Gst fusion protein was generated and immobilized on glutathione-agarose bead matrix (SEPHAROSE; Pharmacia Biotech, Inc., Piscataway, NJ). Proteins capable of binding N-Mena-Gst were then purified from head lysates of stage E12 mouse embryos, or human erythrocytic leukemia cells (HEL). Bound  
20   proteins were analyzed by Western blotting with antibodies to ActA, zyxin, vinculin or the Ack kinase. These and other exemplary studies employing appropriate Gst binding controls demonstrate that N-Mena binds to ActA, zyxin and vinculin, but not to Ack. More specific examples, employing ligand overlay assays using peptides derived from vinculin or ActA (for example according to the methods of Chakraborty et al. EMBO J. 14: 1314-1321, 1995)  
25   demonstrate that N-Mena can associate with motifs common to ActA, zyxin and vinculin.

          The activity of N-Mena and other functional domains of Mena and/or Evl in cytoskeletal dynamic processes can be further evaluated and incorporated within the methods of the invention using a variety of additional tools that are disclosed herein, or are elsewhere described and known in the art. In one example disclosed herein, purified Gst-N-  
30   Mena is microinjected into PtK<sub>2</sub> cells seeded to semi-confluency on CELLocate coverslips (Eppendorf, Hamburg, Germany), and anti-Gst antibody assays coupled with phalloidin labeling to show the distribution of microfilaments is used to demonstrate that the injected

fusion protein localizes to focal adhesions, whereas Gst injected alone is diffusely localized throughout the cytoplasm. Subsequently a peptide containing the ActA sequence SEPSSFEPPTDEELRLA (SEQ ID NO: 12) is injected into the cells in an attempt to saturate the N-Mena binding site for ActA. Following the peptide injection, Gst-N-Mena is observed to be depleted from the focal contacts, whereas distribution of the fusion protein is unaffected by injection of an unrelated ActA peptide. Similar competition assays demonstrate depletion of endogenous Mena in ActA peptide injected cells. These examples and other examples provided herein establish that the EVH1 functional domain of Mena is necessary and sufficient for directing Mena and N-Mena based fusion proteins to focal adhesions and other sites associated with cytoskeletal dynamic processes via direct protein:protein interactions with zyxin, vinculin or other focal adhesion proteins containing an ActA-like motif.

The activity of Mena or Evl and N-Mena and other functional domains of Mena and/or Evl in cytoskeletal dynamic processes can be further evaluated and incorporated within the methods of the invention with the aid of protein crystallography. The basic protein expression methods of the invention provide for the production of sufficiently large amounts of pure Mena and Evl protein to allow crystallographic analysis of Mena and Evl bound and unbound to their various binding partners. These studies will further elucidate the complex structure and function of the Mena and Evl proteins and will be of substantial value in the design of small molecule inhibitors of these proteins.

The activity of N-Mena and other functional domains of Mena and/or Evl in cytoskeletal dynamic processes can be further evaluated and incorporated within the methods of the invention in the context of pathogenic induction of cytoskeletal dynamic processes. In one example disclosed herein involving microfilament induction by the cytopathogenic bacterium *Listeria*, purified Gst-N-Mena was microinjected into PtK<sub>2</sub> cells which were then infected with *Listeria*. Anti-Gst immunoassay coupled with phalloidin labeling shows that the Mena based fusion protein associates with the surface of the bacteria and overlaps with actin in the region of actin polymerization at the tail of the bacterium, similar to the distribution of endogenous Mena in *Listeria* infected cells. Further exemplary studies show that Mena protein translated *in vitro* binds immobilized profilin, which binding is reduced by six-fold following pre-incubation of the profilin matrix with a (GP)<sub>3</sub> peptide (SEQ ID NO: 12) corresponding to the profilin-binding motif of VASP (Reinhard et al.,

EMBO J. 14: 1583-1589, 1995, which is incorporated herein by reference in its entirety). These examples and other examples provided herein establish that the EVH1 functional domain of Mena is necessary and sufficient for directing Mena and N-Mena based fusion proteins to the surface of *Listeria* at the region of actin polymerization to form the bacterial comet tail. Further, these examples establish that Mena contains two distinct domains capable of mediating interactions with ActA, or profilin in association with cytoskeletal dynamic processes required for *Listeria* pathogenicity.

The general methods and compositions described above for localizing and quantifying Mena or Evl associated with dynamic cytoskeletal structures or events, and for determining Mena activity in association with specific factors and events involved in cytoskeletal regulation, provides the basis for a variety of methods to diagnose and treat abnormal cytoskeletal processes associated with pathogenic infection, disease and other conditions, and to screen for agonists and antagonists of specific Mena activities involved in such processes. A particularly useful set of tools in this context includes the various antibodies provided within the invention for detecting Mena and/or Evl expression, activity and localization. Antibody reagents useful for these purposes include antibodies, antibody derivatives and chimeric antibodies that bind to one or more of the Mena and Evl proteins and isoforms thereof. Also provided are antibodies, antibody derivatives and chimeric antibodies that bind to one or more of the Mena or Evl based synthetic peptides, recombinantly produced peptides, fusion proteins and the like disclosed herein.

General methods for the production of non-human antisera or monoclonal antibodies (e.g., murine, lagormorpha, porcine, equine) are well known and may be accomplished by, for example, immunizing an animal with Mena protein or Mena based peptides or alternatively with Evl protein or Evl based peptides. Within one example, for the production of monoclonal antibodies to Mena, antibody producing cells are obtained from immunized animals, immortalized and screened, or screened first for the production of an antibody that binds to the Mena protein or peptides and then immortalized. It may be desirable to transfer the antigen binding regions (i.e., F(ab')<sub>2</sub> or hypervariable regions) of non-human antibodies into the framework of a human antibody by recombinant DNA techniques to produce a substantially human molecule. Methods for producing such "humanized" molecules are generally well known and described in, for example, U.S. Patent No. 4,816,397; which is incorporated by reference herein in its entirety.

Alternatively, a human monoclonal antibody or portions thereof may be identified by first screening a human B-cell cDNA library for DNA molecules that encode antibodies that specifically bind to Mena according to the method generally set forth by Huse et al.

(Science 246: 1275-1281, 1989, which is incorporated by reference herein in its entirety).

- 5 The DNA molecule may then be cloned and amplified to obtain sequences that encode the antibody (or binding domain) of the desired specificity.

Anti-Mena or anti-Evl antibodies are particularly useful within the invention as labeled reagents to detect, image and/or quantify the presence or activity of Mena or Evl, or of agonists or antagonists of Mena or Evl activity. In this context, anti-Mena and anti-  
10 Evl antibodies are provided which incorporate one or more well known labels such as a dye, fluorescent tag or radiolabel. Anti-Mena or anti-Evl antibodies may also be used themselves as agonists or antagonists of Mena or Evl activity, for example by interfering with the binding of Mena to ActA, profilin, zyxin or vinculin. In addition, anti-Mena or anti-Evl antibodies may be used as targeting agents for the delivery of compounds of  
15 therapeutic interest. Such compounds include, but are not limited to, toxins, cytostatic compounds, or proenzymes whose potential function is to activate endogenous proenzymes, to activate proenzymes from exogenous sources, or to activate enzyme cleavage sites on prodrugs. Also contemplated within the invention are bifunctional antibodies having independent antigen binding sites on each immunoglobulin molecule (as  
20 disclosed for example in Thromb. Res. Suppl. X: 83, 1990, and in The Second Annual IBC International Conference on Antibody Engineering, A. George ed., Dec. 16-18, 1991), as well as panels of antibodies having differing specificities. Bifunctional antibodies and antibody panels of particular use within the invention include antibodies and panels of antibodies that bind to both Mena and Evl, or to multiple functional domains of the Mena  
25 or Evl protein.

The subject proteins and peptides of the invention are also useful as reagents to detect, image and/or quantify the presence or activity of Mena or Evl, or of agonists or antagonists of Mena or Evl activity, in addition to their usefulness in the preparation of anti-Mena and anti-Evl antibodies. In this context a collection of Mena or Evl proteins  
30 substantially purified are provided, including all of the Mena and Evl is forms disclosed herein. The Mena and Evl proteins produced according to the present invention may be purified using a number of established methods such as affinity chromatography using anti-

Mena or anti-Evl antibodies coupled to a solid support. Additional purification may be achieved using conventional purification means such as liquid chromatography, gradient centrifugation and gel electrophoresis among others. Methods of protein purification are known in the art (see generally, Scopes, R., Protein Purification, Springer-Verlag, NY, 1982, which is incorporated herein by reference) and may be applied to the purification of recombinant Mena or Evl described herein. Thus, Mena and Evl are provided isolated from its natural cellular environment, and substantially free of other cellular proteins. Purified Mena and Evl are provided, where substantially pure Mena and Evl of at least about 50% is preferred, at least about 70-80% is more preferred, and 95-99% or more homogeneity most preferred. Once purified, partially or to homogeneity, as desired, the recombinant Mena and Evl or native Mena and Evl may be used to generate antibodies, diagnostically in assay procedures, etc.

Also provided are Mena or Evl based synthetic peptides, recombinantly produced peptides, fusion proteins and the like incorporating all or a portion of Mena or Evl. Proteins, peptides and fusion proteins of the invention may be selected to include one or more of the Mena or Evl functional domains disclosed herein, as well as mutant analogs of the Mena or Evl protein or polypeptide which exhibit modified biological activity compared to native Mena or Evl proteins and polypeptide domains.

The proteins, peptides and fusion proteins of the invention are provided according to the methods disclosed herein, as well as by additional recombinant, biosynthetic and peptide chemical methods described elsewhere and generally known in the art. Of particular interest among these methods are site directed mutagenic techniques that can be used to generate targeted mutations in specific regions or functional domains of a Mena or Evl based polynucleotide. For example, it will be generally appreciated that site directed mutagenesis within the EVH1 domain encoding portion of *Mena* will yield Mena mutants that are either hyperfunctional or dominant negative with respect to Mena activities attributable to the EVH1 domain, including ActA, zyxin and vinculin binding activities, and subcellular localization of Mena. Such mutants can be useful by themselves in various applications, or combined with other native or mutant peptide sequences, labels or other agents for more specific purposes. For example, an N-Mena mutant having an enhanced ActA, zyxin or vinculin binding activity selective for a specific binding partner can be used to screen for particularly strong or specific antagonists that inhibit that specific binding activity. Likewise,

hyperfunctional *N-Mena* mutants will be particularly useful as gene therapeutic agent to induce or enhance Mena function in impaired systems, such as in the case of a neural injury or wound healing condition. In more detailed examples, hyperfunctional N-Mena mutants can be operably joined to other peptide sequences, labels or chemical agents to achieve a particular therapeutic value. One such chimeric mutant is contemplated having a hyperfunctional N-Mena mutation as well as a dominant negative mutation in the proline rich, profilin binding domain. This particular chimera will compete strongly with endogenous Mena for ActA, zyxin and vinculin binding, but will fail to promote wild type profilin binding and microfilament assembly. Such a mutant will be useful tool in a variety of applications, for example to screen for agonists that replace or enhance Mena-profilin binding activity, or as a gene therapeutic agent capable of inhibiting endogenous Mena function in aberrant migratory cells, such as Chronic Myelogenous Leukemia (CML) and other cancer cells.

In further aspects of the invention, Mena or Evl proteins, peptides, fusion proteins and antibodies are used in a variety of screening and diagnostic methods. As will be evident to the common practitioner, the polynucleotide molecules, protein, peptides and antibodies of the present invention or useful in *in vitro* assays to screen for compounds capable of modulating the activity of expression of Mena or Evl. Within such assays, test compounds may be assessed for their ability to increase or decrease Mena activity or expression relative to a control assay in which the test compound is absent. Screening assays of the present invention exploit the binding of Mena and Evl to different substrates. Within one embodiment, test compounds are screened for the ability to compete with Mena binding partners such as ActA, profilin, Zyxin or Vinculin. Within another embodiment, test compounds are screened for the ability to modulate Mena or Evl activity by increasing or decreasing Mena or Evl expression.

In preferred diagnostic methods, labeled Mena or Evl proteins, peptides, or anti-Mena or anti-Evl antibodies are employed to detect expression, localization and/or activity of Mena or Evl associated with normal and/or abnormal cytoskeletal structures or processes, or in association with specific molecular factors involved in cytoskeletal regulation. In one general diagnostic example, Mena or Evl expression or activity is detected and/or quantified in a normal cell population or tissue, and these results are compared to Mena or Evl expression or activity detected and/or quantified in a test cell population or tissue (for

example a population of cancerous cells or cells from a site of neural injury). Detection and/or quantification of Mena or Evl expression, localization or activity can be accomplished by a variety of methods, such as by in situ hybridization using anti-Mena or anti-Evl antibodies on embryos or tissue sections or within antibody microinjected cells, by Western blotting or immunoprecipitation using anti-Mena or anti-Evl antibodies in cell or tissue lysates, or by affinity purification using anti-Mena or anti-Evl antibodies bound to a solid phase, among other methods. Comparable methods are disclosed herein, or are elsewhere disclosed and known in the art, for using non-antibody agents to detect and/or quantify Mena or Evl expression or activity. Suitable non-antibody probes for use within these methods include for example oligonucleotide probes that hybridize to Mena or Evl transcripts, labeled binding partners of Mena or Evl such as ActA, zyxin, vinculin or profilin, and synthetic or recombinant peptide analogs of Mena or Evl binding partners, among other useful probe types. For example, Mena and Evl cDNA and oligonucleotide probes may be useful in Northern, Southern, and dot-blot assays for identifying and quantifying the level of expression of Mena or Evl in a cell. Measuring the level of Mena or Evl expression may provide prognostic markers for assessing the growth rate and invasiveness of tumors. In addition, considering the role of Mena in axonogenesis, birth defects and abortions may result from the absence or expression of an abnormal Mena protein. In this case, Mena may be useful in prenatal screening of mothers and/or for *in utero* testing of fetuses.

Differences that are detected and/or quantified between Mena or Evl expression or activity between normal and test cell populations or tissues may be diagnostic of particular disease states or other conditions characterized by aberrant cytoskeletal structure or regulation. In the case of cancerous or precancerous test cells, such as CML cells, an increase of Mena expression compared to control cells is predictive of an increased risk of metastatic disease due to Mena-mediated cell motility and reduction of contact inhibition. In the case of test cells taken from sites of neural injury, the level of Mena expression or activity compared to control cells is predictive of the extent of neural regeneration that can be expected in a particular case, and may also be useful for determining preferred courses of treatment. In the case of test cells suspected of carrying *Listeria* infection, or infection by any of a number of other pathogenic agents that induce cytoskeletal dynamic processes in infected cells, the presence and pattern of Mena expression in association with the

pathogen provides a positive diagnosis of the type of infection, and the level of Mena expression or activity compared to control cells is diagnostic of the severity of infection.

Additional diagnostic methods of the invention rely on labeled polynucleotide probes to map the chromosomal locations of Mena, Evl and related genes, to determine linkage of these genes relative to other genes, and to identify genetic defects in these genes among cell populations or individuals. To facilitate these methods, *Mena* was demonstrated by genetic linkage analysis to be located in the mouse to chromosome 1a offset 73 in the Jackson backcross hybrid mapping panel. This location in the mouse is syntenic to a human chromosomal position of 1Q21-23 (Stanier et al., Genomics 26: 473-478, 1995), which location adds significance to the methods of the invention because it is a putative hot spot for breast cancer.

Yet additional diagnostic methods of the invention rely on the detection and/or quantification of phosphorylation of Mena or Evl. Cytoskeletal dynamic processes are mediated by a variety of signal cascades that can be induced by external stimuli such as adhesion through integrins or stimulation with a growth factor such as PDGF. Many of these signals are propagated in part by kinase cascades that may trigger Mena phosphorylation. In this context, it is noteworthy that Src family kinases are concentrated in neuronal growth cones (Bixby and Jhabvala, J. Neurosci. 13, 3421-32, 1993), and c-Src may be required for proper neurite outgrowth on the cell adhesion molecule L1 (Ignelzi et al., Neuron 12:, 873-84, 1994). Mammalian c-Abl is another logical candidate Mena kinase. From studies in NIH3T3 cells, c-Abl is widely perceived as a largely nuclear tyrosine kinase. However, in P19 neurons, Abl is found exclusively in the cytoplasm and in growth cones. A role for cytoplasmic c-Abl in actin dynamics is indicated by the presence of G- and F-actin binding activities in its C-terminus (McWhirter et al., Mol. Cell. Biol. 13, 7587-95, 1993; McWhirter et al., Mol. Cell. Biol. 11, 1553-1565, 1991; McWhirter and Wang, EMBO J. 12, 1533-1546, 1993; Van Etten et al., J. Cell. Biol. 124, 325-340 1994). Evaluating the potential involvement of Mena in normal c-Abl function, and in neoplasias induced by Abl oncogenes, is an important object of the invention. In this context, it is shown herein that Mena contains serine residues aligning to known cyclic nucleotide kinase-dependent phosphorylation sites in VASP (Butt et al., J. Biol. Chem. 269: 14509-17, 1994). These serine residues in Mena flank the central proline-rich region of the protein. Evl contains the amino-terminal site only, while Ena lacks both sites. In



the examples below it is also shown that a slower migrating form of Mena is less efficiently recovered in SH3 binding assays than a faster form. These and other data suggest that some interactions mediated by the proline-rich core of Mena may be regulated by post-translational modification of the protein, such as serine-threonine phosphorylation.

- 5 Tyrosine phosphorylation of the larger, neural isoform of Mena may promote interactions with molecules that contain SH2 or PTB domains and link Mena to other signaling complexes. In addition, the alternatively-included portions of the 140 kD Mena isoform may contain the phosphorylated tyrosine(s), or sequences that recruit Mena kinases. These findings indicate that diagnostic and screening methods of the invention will be
- 10 useful to identify and characterize any cytoskeletal dynamic processes involving Mena or Ena phosphorylation, to diagnose defects in such processes, and to screen for modulators of such processes that may be useful in therapeutic and other applications.

- The same steps and compositions that are employed within diagnostic methods of the invention are readily adapted for use within powerful screening methods provided by the
- 15 invention. Screening methods that are particularly useful within the invention include high throughput screening assays designed to identify modulators of Mena or Evl expression or activity. In preferred screening assays, labeled Mena or Evl proteins, peptides, or anti-Mena or anti-Evl antibodies are employed in a similar manner as described above to detect and/or quantify expression or activity of Mena or Evl in comparable test and control samples.

- 20 Useful control samples in this context generally include a variety of *in vivo* or *in vitro* assay mixtures suitable for detecting and/or quantifying Mena or Evl binding to a selected binding partner, for example ActA, zyxin, vinculin or profilin. Other suitable control samples include *in vivo* or *in vivo* assays mixtures suitable for detecting other activities of Mena or Evl, for example subcellular localization of Mena to the surface of a cytopathogenic bacteria or a site
- 25 of endogenously controlled microfilament formation, or Mena or Evl phosphorylation.

- Useful test samples within these screening methods contain an added test substance, i.e. a putative Mena or Evl modulating agent, in qualitatively or quantitatively comparable assay mixtures to those of the control samples. In screens aimed at detecting modulators of Mena or Evl binding to a selected binding partner, the test sample contains suitable amounts of
- 30 Mena or Evl protein and a selected binding partner under conditions that permit the formation of Mena- or Evl-binding partner complexes in the absence of the test substance. The complexes are then detected and/or quantified according the methods disclosed herein,

and these results are compared to the results of detection and/or quantification of Mena- or Evi-binding partner complexes formed in the control sample.

Also provided are kits and multicontainer units comprising reagents and components for practicing the assay methods of the present invention. Kits of the present invention may, in addition to reagents for detecting Mena and Evi, contain enzymatic reagents such as reverse transcriptase or polymerase; suitable buffers; nucleoside triphosphates; suitable labels for labeling the reagents for detecting Mena and Evi and developing reagents for detecting the signal from the label. In one aspect, kits of the present invention contain sequence-specific oligonucleotide primers for detecting polynucleotide molecules encoding Mena and Evi. Such primers may be provided in separate containers or may be provided in combinations of one or more primer pairs in a series of containers. One aspect of the invention provides kits containing Mena and Evi sequence-specific probes. Within yet another aspect, kits contain antibodies useful for detecting Mena and Evi (or mutants thereof) in a sample. Such kits contain Mena- and/or Evi-specific antibodies for detecting Mena and Evi protein. The Mena and Evi-specific antibodies may be labeled or may be detected by binding to a secondary antibody. The antibody reagents may be provided in separate container or may be provided in combination in a series of containers. In addition to these components, the kits may also contain instructions for carrying out the assay and/or additional containers suitable for carrying out the reactions of the assay.

The complex structure of the Mena and Evi proteins, and the various biological activities of EVH1 and other functional domains of Mena or Evi, provide for a broad array of potential screening assays and assay formats. Among these various screening methods ligand binding assays using immobilized Mena or Evi proteins or fusion proteins are preferred for high throughput screening purposes. In one such method, labeled Mena or Evi proteins or Mena or Evi based peptides or fusion proteins are immobilized on a solid phase, for example, an N-Mena-Gst fusion protein immobilized on a glutathione-agarose bead matrix such as glutathione SEPHAROSE (Pharmacia Biotech, Inc., Piscataway, NJ). The control assay sample is completed by exposing the bound N-Mena-Gst fusion protein to a N-Mena ligand, for example ActA, zyxin or vinculin. The ligand may be provided in a purified form, or as a component of a ligand-containing mixture, for example a cell or tissue lysate. N-Mena-ligand complexes are detected and/or quantified following exposure of the ligand to the bound fusion protein using any of a variety of detection or quantification methods

disclosed herein, for example by a selected immunoassay using antibodies to ActA, zyxin or vinculin. The test assay sample is prepared in a comparable fashion, by exposing the bound N-Mena-Gst fusion protein to an N-Mena ligand under conditions that permit formation of N-Mena-ligand complexes in the control assay sample. However, prior to detection and/or quantification of N-Mena-ligand complexes in the control assay sample, a test substance is included therein. Generally the test substances is added in the form of a purified agent, however it is also contemplated that test substances useful within the invention may include substances present throughout the handling of test sample components, for example host cell factors that are present in a cell lysate used for generating the test sample. Such endogenous factors may be segregated between the test and control samples for example by using different cell types for preparing lysates, where the cell type used for preparing the test sample expresses a putative test substance that is not expressed by the cell type used in preparing the control sample. A particularly useful set of test and control cell types in this context are P19 embryonic carcinomal cells that have and have not been induced to undergo neural differentiation by retinoic acid.

More specific screening methods of the invention are also disclosed herein, including ligand overlay assays using peptides derived from Mena or Evl binding partners as test substances (for example according to the methods of Chakraborty et al. EMBO J. 14: 1314-1321, 1995) in assay mixtures and under suitable conditions that permit binding of Mena or Evl to the same or different binding partner in the control sample. In other screening assays, test and control samples include reagents that are microinjected into cells to yield an *in vivo* assay mixture. In one such method, Gst-N-Mena is microinjected into PtK<sub>2</sub> cells seeded to semi-confluency on CELLocate coverslips (Eppendorf, Hamburg, Germany). Labeled anti-Gst or anti-N-Mena antibodies are also injected or otherwise delivered (e.g. by microporation or liposomal transfection) into the cells. In a control sample of cells thus treated, the pattern and/or intensity of antibody labeling is detected. In the test sample, a test substance such as the ActA sequence SEPSSFEPPTDEELRLA (SEQ ID NO: 12), is delivered into the cell prior to detecting the pattern and/or intensity of antibody labeling. Results of this form of assay can be readily determined based on simple qualitative observations, for example by immunofluorescence visualization of Gst-N-Mena depletion from focal contacts, or from the surface of *Listeria* or other pathogens in infected cells, confined to the test sample.

Screening for modulators of Mena or Evi expression or activity in the context of pathogenic infection is a particularly useful method, both in terms of the simplicity of the assay systems available, as well as in terms of the anticipated utility of the modulators that may be uncovered in such screens. In this context it is important to note that the *Listeria monocytogenes* organism is only one of many diverse pathogens that rely on the induction of host cytoskeletal dynamic processes for pathogenicity. The ability to grow in a host cell cytoplasm accompanied by actin-based movement and cell-to-cell spreading has also been observed for the closely related pathogen *Listeria ivanovii* and is shared by two other groups of pathogenic bacteria, *Shigella flexneri* and *Rickettsia conorii* and *Rickettsia rickettsii* (reviewed in Chakraborty et al. EMBO J. 14: 1314-21, 1995). In *S. flexneri*, a gene encoding an outer membrane protein variously denoted VirG or IcsA has been identified and is required for host actin recruitment to form actin halos and comets to spread from cell to cell (Pollard, Current Biology 5: 837-40, 1995, which is incorporated herein by reference in its entirety). In addition to these pathogens which appear to share closely related actin recruitment mechanisms, there are a variety of different pathogens having apparently distinct mechanisms and/or used for host cell actin recruitment. Among these organisms, the often lethal enteropathogenic *E. coli* (EPEC) and the pathogenic enterohemorrhagic form of *E. coli* (EHEC) have the ability to induce host cell tyrosine kinases and actin accumulation leading to profound host cytoskeletal disruption (reviewed by Donnenburg et al., J. Clin. Invest. 92: 1418-24, 1995, which is herein incorporated by reference in its entirety). In addition, diverse viral pathogens have recently been discovered to also cause profound changes in cytoskeletal dynamic processes. For example, the HIV virus spreads between cells via syncytia formation which involves both cell motility and reorganization of the cytoskeleton accompanied by condensation of F-Actin (Sylwester et al., J. Cell. Sci. 106: 941-53, 1993, which is herein incorporated by reference in its entirety). Likewise, vaccinia virus in its intracellular enveloped form induces the formation of actin tails that are "strikingly similar" to those seen in *Listeria*, *Shigella* and *Rickettsia* infections (Cudmore et al., Nature 378: 636-8, 1995, which is herein incorporated by reference in its entirety). Considering the diversity and widespread occurrence of pathogenic cytoskeletal induction mechanisms, and in view of the particularly deleterious impacts of known pathogens that employ these mechanisms against humans and other mammals, the screening methods of the invention will be particularly useful to identify negative modulators of Mena or Evi

expression and/or activity. Once identified, these Mena or Evl inhibitors will supplement existing tools and methods within the invention for preventing and treating such pathogenic diseases.

A variety of other screening methods are made available within the invention which  
5 rely on the construction of recombinant cell lines, ova, transgenic embryos and animals transformed to include mutant forms of the Mena or Evl genes, including dominant-negative and "knock-out" recombinants in which the activity of Mena or Evl protein is down-regulated or eliminated. Generally, *Mena* or *Evl* based recombinant polynucleotide expression constructs are provided which include a polynucleotide insert encoding a Mena  
10 or Evl protein or peptides, fusion protein or the like operably incorporated within an expression vector capable of directing expression of the polynucleotide insert in a mammalian host cell. Such constructs may include native or mutagenized forms of the Mena or Evl protein or of selected polypeptide portions of Mena or Evl such as the EVH1 functional domain. Various such constructs are provided, including constructs that  
15 incorporate polynucleotide sequences encoding the native 140 kD, 60 kD, 80 kD or 88 kD Mena isoforms, Evl or consensus sequences derived from SEQ ID NO: 9. Cells transformed with these constructs may contain for example altered *Mena* coding sequences that result in the expression of a Mena protein that is not capable of binding to one or more of the EVH1 domain ligands of Mena, including ActA, zyxin and vinculin, or which has enhanced binding  
20 to profilin that results in a phenotype characterized by hyperfunctional actin polymerization. The subject cell lines and animals find uses in screening for candidate therapeutic agents capable of either substituting for a function performed by Mena or correcting the cellular defect caused by a defective Mena. In addition, the polynucleotide molecules of the present invention may be joined to reporter genes, such as  $\beta$ -galactosidase or luciferase, and inserted  
25 into the genome of a suitable embryonic host cell such as an mouse embryonic stem cell by, for example, homologous recombination (for review, see Capecchi, Trends in Genetics 5: 70-76, 1989; which is incorporated by reference). Cells and cell lines expressing the subject molecules may then be obtained and used, for example, for screening for compounds that increase or decrease expression of the reporter gene.

30 In one such example discussed in more detail below, "knock-out" mice are generated by replacing the murine *Mena* or *Evl* coding region with the  $\beta$ -galactosidase reporter gene and the neomycin resistance gene to assess the consequences of eliminating the murine Mena

or *Evl* protein, and to examine the tissue distribution of *Mena* or *Evl* in fetal and post-natal mice. These "Knock out" mice are useful for example as model systems for screening compounds that may developmentally, spatially and/or quantitatively alter the expression of the reporter gene. Such mice may be used to study methods to rescue homozygous mutants  
5 and as hosts to test transplant tissue for treating diseases or other conditions characterized by aberrant regulation of cytoskeletal dynamic processes.

In addition to the screening and diagnostic methods disclosed herein, the invention provides a range of therapeutic methods for preventing and/or treating diseases and other conditions that involve aberrant cytoskeletal regulation, for example pathogenic infection,  
10 traumatic neural injury and cancer. Therapeutic methods of the invention variously utilize *Mena* or *Evl* encoding polynucleotides, *Mena* or *Evl* proteins and peptides, *Mena* or *Evl* binding antibodies, *Mena* or *Evl* based expression constructs, mammalian host cells transformed to express *Mena* or *Evl* insert sequences, and other therapeutic agents generally characterized as modulators of *Mena* or *Evl* expression or activity, including  
15 triplex forming oligonucleotides, antisense polynucleotides and ribozymes that specifically target *Mena* and/or *Evl* polynucleotides.

In preferred therapeutic methods directed to the treatment of pathogenic infection and cancer, it is useful to employ agents that inhibit *Mena* or *Evl* expression or activity and which thereby can eliminate or impair aberrant recruitment of *Mena* by pathogens, or  
20 interrupt *Mena* expression or activity associated with cancerous cell migration. In preferred therapeutic methods directed to the treatment of traumatic neural injury and other injury conditions where it is desirable to promote cell migration for neural regeneration or wound healing, it is useful to employ agents that induce or enhance *Mena* or *Evl* expression or activity. Useful agents in this context generally include agents that  
25 enhance *Mena* or *Evl* binding to its partners or otherwise enhance *Mena* or *Evl* expression or activity, for example mutant *Mena* or *Evl* based expression constructs that induce or enhance *Mena* or *Evl* expression or activity in targeted cells.

Therapeutic substances which can serve as inhibitors or antagonists of *Mena* or *Evl* include, but are not limited to, compounds capable of inhibiting the formation of *Mena*-  
30 profilin or *Mena*-proline-rich binding partner, compounds that reduce or inhibit the activity of *Mena*, and compounds that interfere with the expression of *Mena* protein. Such agents may include chemical compound inhibitors of *Mena*, protein or peptide *Mena* antagonists,

and molecules that inhibit the expression of Mena such as triplex forming oligonucleotides, antisense polynucleotides, ribozymes, etc..

The use of antisense polynucleotides and their applications are described generally in, for example, Mol and Van der Krul, eds., Antisense Nucleic Acids and Proteins  
5 Fundamentals and Applications, New York, NY, 1992, which is incorporated by reference herein in its entirety. Suitable antisense oligonucleotides are at least 11 nucleotides in length and up to and including the upstream untranslated and associated coding sequences of Mena. As will be evident to one skilled in the art, the optimal length of antisense oligonucleotides is dependent on the strength of the interaction between the antisense oligonucleotides and their  
10 complementary sequence on the mRNA, the temperature and ionic environment in which translation takes place, the base sequence of the antisense oligonucleotide, the presence of secondary and tertiary structure in the mRNA and/or in the antisense oligonucleotide and the preferred delivery mode. For example, soluble antisense oligonucleotides have been used to inhibit transcription/translation of a target gene (Ching et al., Proc. Natl. Acad. Sci. U.S.A.  
15 86:10006-10010, 1989; Broder et al., Ann. Int. Med. 113: 604-618 (1990); Loreau et al., FEBS Letters 274:53-56 1990; Holcenberg et al., WO91/11535; U.S.S.N. 07/530,165 ("New human CRIPTO gene"); WO91/09865; WO91/04753; WO90/13641; and EP 386563, each of which is incorporated herein by reference). Suitable target sequences for antisense polynucleotides include intron-exon junctions (to prevent proper splicing), regions  
20 in which DNA/RNA hybrids will prevent transport of mRNA from the nucleus to the cytoplasm, initiation factor binding sites, ribosome binding sites, and sites that interfere with ribosome progression. A particularly preferred target region for antisense polynucleotides is the 5' untranslated region of the gene of interest, for example the *Mena* gene.

Antisense polynucleotides targeted to the Mena gene may also be prepared by  
25 inserting a DNA molecule containing the target DNA sequence into a suitable expression vector such that the DNA molecule is inserted downstream of a promoter in a reverse orientation as compared to the gene itself. The expression vector may then be transduced, transformed or transfected into a suitable cell resulting in the expression of antisense polynucleotides. Alternatively, antisense oligonucleotides may be synthesized using standard  
30 manual or automated synthesis techniques. Synthesized oligonucleotides may be introduced into suitable cells by a variety of means including electroporation (e.g., as described in Yang et al., Nucl. Acids. Res. 23:2803-2810, 1995), calcium phosphate precipitation,

microinjection, poly-L- methine/DMSO (Dong et al., Nucl. Acids. Res. 21:771-772, 1993). The selection of a suitable antisense oligonucleotide administration method will be evident to one skilled in the art. With respect to synthesized oligonucleotides, the stability of antisense oligonucleotide-mRNA hybrids may be increased by the addition of stabilizing agents to the oligonucleotide. Stabilizing agents include intercalating agents that are covalently attached to either or both ends of the oligonucleotide. Oligonucleotides may be made resistant to nucleases by, for example, modifications to the phosphodiester backbone by the introduction of phosphotriesters, phosphonates, phosphorothioates, phosphoroselenoates, phosphoramidates or phosphorodithioates. Oligonucleotides may also be made nuclease resistant by the synthesis of the oligonucleotides with alpha-anomers of the deoxyribonucleotides, as generally described in Mol and Van der Krul, *supra*.

Within another embodiment, polynucleotide-based inhibitors of the present invention include the triplex forming oligonucleotides, sequence-specific DNA binding drugs that interfere with target gene transcription. Triplex-forming oligonucleotides are generally described in Maher, Bioessays 14: 807-815, 1992; Gee et al., Gene 149: 109-114, 1994; Noonberg et al., Gene 149: 123-126, 1994; Song et al., Ann. NY Acad. Sci. 761: 97-108, 1995; Westin et al., Nuc. Acids. Res. 23: 2184-2191, 1995; and Wand and Glazer, J. Biol. Chem. 207: 22595-22901, 1995. These oligonucleotides form triple helical complexes under physiological conditions on double-stranded DNA, selectively inhibiting gene transcription by physically blocking RNA polymerase or transcription factor access to the DNA template. See also, e.g., WO 95/25818; WO 95/20404; WO 94/15616; WO 94/04550; and WO 93/09788, each of which is incorporated herein by reference. The triplex forming oligonucleotides may contain either a nucleotide or non-nucleotide tail to enhance the inhibition of transcription factor binding. Within one example, the triplex forming oligonucleotides are targeted to the *Mena* gene.

For polynucleotide-based inhibitors, the choice of a suitable sequence will be guided by, for example, the type of inhibitor (i.e., triplex forming oligonucleotide or antisense polynucleotide) and the species to be treated. It may be preferable to choose sequences that are conserved between species to permit use in readily available animal models.

The present invention also provides compositions and methods for using ribozyme inhibitors for inhibiting Mena expression. The ribozymes can be administered in a variety of ways, including by gene therapy targeted to a desired cell. A ribozyme of the invention is a



targets the RNA transcripts of the gene of interest in a sequence-specific manner. For example, ribozymes may be designed to specifically inhibit the transcription of the *Mena* gene. Each ribozyme molecule is designed to contain a catalytically active segment capable of cleaving the *Mena* RNA, and further comprises flanking sequences having a nucleotide sequence complementary to portions of the targeted RNA. The flanking sequences serve to anneal the ribozyme to the RNA in a site-specific manner. Absolute complementarity of the flanking sequences to the target *Mena* sequence is not necessary, however, as only an amount of complementarity sufficient to form a duplex with the target RNA and to allow the catalytically active segment of the ribozyme to cleave at the target sites is necessary. Thus, only sufficient complementarity to permit the ribozyme to be hybridizable with the target RNA under physiological conditions is required.

As used herein, the term "ribozyme" means an RNA molecule having an enzymatic activity that is able to cleave or splice other separate RNA molecules in a nucleotide base sequence specific manner. By reference to catalytic or enzymatic RNA molecule is meant an RNA molecule which has complementarity in a substrate binding region to a specific RNA target (e.g. *Mena* RNA), and also has enzymatic activity that is active to cleave and/or splice RNA in that target, thereby altering the target molecule. In preferred embodiments of the present invention the enzymatic RNA molecule is formed in a hammerhead motif, but the ribozyme may also be formed in the motif of a hairpin, hepatitis delta virus, group I intron or RNase P RNA (in association with an RNA guide sequence). Examples of hammerhead motifs are described by Rossi et al., AIDS Res. Hum. Retrovir. 8: 183 (1992), hairpin motifs are described by Hampel et al., Biochem. 28:4929 (1989) and Hampel et al., Nucl. Acids Res. 18: 299 (1990), the hepatitis delta virus motif is exemplified in Perrotta and Been, Biochem. 31: 16 (1992), an RNaseP motif is described in Guerrier-Takada et al., Cell 35: 849 (1983), and examples of the group I intron motif are described in Cech et al., U.S. Patent 4,987,071, each of the foregoing disclosures being incorporated herein by reference. These specific motifs are not limiting in the present invention and those of skill in the art will recognize that an enzymatic RNA molecule of the invention has a specific substrate binding site which is complementary to one or more of the target RNA regions and that it has nucleotide sequences within or surrounding that substrate binding site which impart an RNA cleaving activity to the molecule.

The flanking sequences upstream and downstream of the ribozyme catalytic site may comprise segments of any length that effectively imparts the desired degree of targeting specificity for the ribozyme. Preferably a flanking sequence comprises from about 4 to about 24 nucleotides, more preferably from about 6 to about 15 nucleotides, and typically about 9 to 12 nucleotides, and results in base pairing to the substrate sequence immediately upstream and downstream of the RNA sequences which comprise the cleavage site.

The Mena or Evi modulating agents, including Mena and Evi inhibitors and agonists, of the present invention may be used in a variety of therapeutic contexts, alone or in combination, and may be formulated for a variety of modes of administration.

Administration of the inhibitor or agonist may include systemic, topical or local administration. Techniques and formulations are generally described in Remington's Pharmaceutical Sciences, Mack Publishing Co., Easton, PA, latest edition. The inhibitor or agonist is generally combined with a pharmaceutically acceptable carrier such as a diluent or excipient. Suitable carriers may include fillers, extenders, binders, wetting agents, disintegrants, surface-active agents or lubricants. The choice of such ingredients will depend on the mode of administration and dosage forms. Typical dosage forms include tablets, powders, liquid preparation including suspensions, emulsions, and solutions, granules, capsules and suppositories. Liquid preparation for injection are also typical and include liposome preparations.

Polynucleotide inhibitors, e.g., triplex forming oligonucleotides, antisense oligonucleotide, ribozyme, etc., or a combination of such inhibitors targeted to different portions of the target DNA or corresponding RNA can be delivered in a wide variety of ways to targeted cells to facilitate inhibition of the gene of interest. Within one example, multiple polynucleotide inhibitors of *Mena* are combined and delivered to target cells to decrease the expression of Mena, thus reducing the recruitment of Mena to, for example, focal adhesions. The oligonucleotides can be administered as synthetic oligonucleotides or expressed from an expression vector. The oligonucleotide can be administered *ex vivo*, i.e., contacted with target cells that have been removed from an individual or other cell source, treated and returned, or the oligonucleotide molecule can be administered *in vivo*. When administered *ex vivo* typically the target cells are exposed to mitogens, e.g., serum mitogens (SCF, IL-3, EPO, TPO, etc.) or the like depending on the particular cell population.

Delivery of inhibitors or agonists to a targeted cell population can be via a wide range of available delivery vehicles, e.g., a liposome, a controlled release vehicle, by use of iontophoresis, electroporation or ion paired molecules, or covalently attached adducts, and other pharmacologically acceptable methods of delivery. Preferably a carrier provides a means to accumulate the inhibitor or agonist within or at a desired cell population. The delivery vehicle can be designed to serve as a slow release reservoir or to deliver its contents directly to the target cell. Examples of oligonucleotide delivery vehicles include liposomes, hydrogels, cyclodextrins, biodegradable nanocapsules, and microspheres. Liposomes can readily be targeted to the various tissues or cell populations.

For in vivo use, routes of administration for Mena or Evi inhibitors and agonists include intramuscular, aerosol, intravenous, parenteral, intraperitoneal, etc. The specific delivery route for a selected inhibitor or agonist will depend on a variety of factors, such as the form of the inhibitor or agonist, the intended target, the condition being treated, etc. For example, while unmodified oligonucleotide is taken up by cells, modifications can be made to enhance cellular uptake, e.g., by reducing the oligonucleotide's charge to produce a molecule which is able to diffuse across the cell membrane. The structural requirements necessary to maintain oligonucleotide activity and activity of other classes of inhibitors or agonists are generally recognized in the art. Modifications to enhance cellular delivery can also be designed to reduce susceptibility to nuclease digestion or other types of degradation.

The dosage of inhibitor or agonist will also depend on a variety of factors, such as the form of the inhibitor or agonist, the route of administration, etc., and thus can vary widely. Generally the dosage of inhibitors will result in inhibition of *Mena* activity or levels to a sufficient extent within the targeted cells sufficient to prevent formation of *Mena* complexes with its binding partners. Establishment of effective levels of inhibitor within a targeted cell population depends upon, e.g., the rate of uptake (or expression by a particular vector), and rate at which the inhibitor is degraded. The duration of treatment may extend for a time sufficient to permit, e.g., transduction of a relatively high percentage of dividing cells compared to an untreated control cell population, but usually will be at least for about 2-4 days, sometimes 6-10 days, although longer durations may be necessary for quiescent or terminally differentiated cell populations. The number and timing of doses can vary considerably, depending on the factors discussed above and the efficacy of a particular inhibitor or mixture thereof, the delivery vehicle and route of administration, etc.

For oligonucleotide inhibitors of the present invention, for example Mena antisense oligonucleotide inhibitors or Mena-specific triplex forming oligonucleotides, it may be preferable to include an effective concentration of a lipid formulation with the oligonucleotide. Suitable lipid formulations and concentrations are those that enhance the uptake of the oligonucleotides by cells. Such lipids include cationic lipids used for lipofection such as N- [1-(2,3-dioleoyloxy)propyl]-N,N,N-trimethylammonium chloride (DOTMA) and dioleoyl phosphatidylethanolamine (DOPE). One skilled in the art may determine the particular lipid formulation or concentration that will be effective for enhancing the uptake of the oligonucleotide.

Within the methods described in detail herein, Mena or Evt inhibitors or agonists may be used in combination with other compounds that are useful, for example in chemotherapy or as antibiotics. These compounds include standard chemotherapeutic agents such as platinum compounds (e.g. cisplatin) and antibiotics such as penicillin, tetracycline or antiviral agents such as protease inhibitors and the like.

Within additional aspects of the invention, the *Mena* or *Evt* based polynucleotide expression constructs disclosed herein are employed in methods for modulating the expression of *Mena* or *Evt*, disrupting *Mena* or *Evt* expression or inducing ectopic expression of *Mena* or *Evt* genes and related polynucleotide sequences in the context of gene therapeutic methods involving mammalian host cells. In preferred gene therapeutic methods of the invention, Mena is ectopically expressed or over expressed in mammalian cells to induce cytoskeletal changes, including for example formation of dense F-actin clusters, cell surface protrusions characterized by Mena-actin core structures, and filopodial extension and cytoplasmic bridge formation between neighboring cells.

Introduction of the subject nucleotide sequences into cells may be accomplished *in vitro* or *in vivo* using a suitable gene therapy vector delivery system (e.g., a retroviral vector), a microinjection technique (see, for example, Tam, Basic Life Sciences 37: 187-194, 1986, which is incorporated by reference herein in its entirety), or a transfection method (e.g., naked or liposome encapsulated DNA or RNA) (see, for example, Trends in Genetics 5: 138, 1989; Chen and Okayama, Biotechniques 6: 632-638, 1988; Mannino and Gould-Fogerite, Biotechniques 6: 682-690, 1988; Kojima et al., Biochem. Biophys. Res. Comm. 207: 8-12, 1995; which are incorporated by reference herein in their entirety). Gene transfer vectors (e.g., retroviral vectors, and the like) may be constructed wherein a

polynucleotide molecule of the invention is inserted into the vector under the control of a promoter. Gene therapy may be used to correct traumatic neural injury that has resulted in loss of motor or sensory neural function. The introduction method may be chosen to achieve a transient expression of Mena in the host cell, or it may be preferable to achieve  
5 constitutive, tissue specific, or inducible expression.

Methods of treatment employing transformed host cells of the present invention are useful in a variety of *in vivo* settings, for example, for transplantation at sites of traumatic neural injury where motor or sensory neural activity has been lost. The polynucleotide constructs and insert sequences of the invention provide the possibility of specific gene  
10 therapy for the treatment of certain neurological disorders such as Alzheimer's disease, Huntington's disease, and Parkinson's disease, in which a population of neurons have been damaged. Representative patient populations that may benefit from transplantation include, but are not limited to, patients with hearing or vision loss due to optical or auditory nerve damage, patients with peripheral nerve damage and loss of motor or  
15 sensory neural function, individuals with diseases such as cancer or developmental defects relating to aberrant cytoskeletal dynamic function, and patients with brain or spinal cord damage from traumatic injury. In one example, donor cells for a patient having CML are obtained from a normal stem cell population in the same patient or in a donor patient and are then transformed or transduced with a mutant *Mena* or *Evl* nucleotide sequence. A  
20 preferred *Mena* mutant in this context can be designed to express a hyperfunctional EVH1 domain that has a strongly enhanced binding affinity for ligands such as zyxin or vinculin that mediate Mena function in cytoskeletal dynamic processes. To render this mutant effective as an antagonist of native Mena function in the transformed donor cells, a second mutation can be introduced in a separate functional domain, for example the proline rich,  
25 profilin binding domain, that renders the double mutant protein incapable of binding profilin to promote actin polymerization, while it remains tightly bound to its EVH1 domain ligands and thereby prevents or impairs binding and function of endogenous Mena in the donor cells. The transformed cells that are rendered resistant to the motility defects and loss of contact inhibition of CML cells are then returned to the patient, for example in  
30 the manner routinely performed during bone marrow transplants. Alternatively, gene transfer may be achieved by introducing the sequences of the present invention directly to the site of the traumatic injury.

The following examples are offered by way of illustration, not by way of limitation.

### Example 1

#### Cloning of Mena and Evi

5 A cDNA encoding Mena was identified by screening a cDNA library made from mouse embryonic stem cells (Chen et al., Proc. Natl. Acad. Sci. USA 92: 7819-7823, 1994). Filter lifts of the library were prepared on nylon membranes (HYBOND, Amersham, Arlington Heights, IL). Library screening, subcloning and polymerase chain reactions were performed, and standard solutions prepared essentially as described by  
10 Sambrook et al. (Molecular Cloning: A Laboratory Manual, Cold Spring Harbor, NY, 1989, which is incorporated herein by reference in its entirety). The library was screened with a <sup>32</sup>P-labeled (Amersham, Arlington Heights, IL) Eco R1/Sph I fragment containing the first 106 codons of Ena (Gertler et al., Genes Dev. 9: 521-533, 1995). The filters were hybridized in a buffer containing: 1.5 x SSPE, 7% SDS, 10% PEG8000 and 1x10<sup>6</sup> cpm/ml  
15 of the <sup>32</sup>P-labeled Ena probe overnight at 42°C. The filters were washed repeatedly at 42°C in a buffer containing 2 x SSC, 1% SDS followed by washes at 60°C in a buffer containing 0.5 x SSC, 1% SDS.

Positive phage were identified by autoradiography and purified. The cDNA inserts were subcloned into pBSKSII (Stratagene Cloning Systems, La Jolla, CA). The inserts  
20 were prepared and sequenced on both strands using an Applied Biosystems DNA Sequencer model 373A (Applied Biosystems, Foster City, CA) according to the manufacturer's guidelines. Analysis of overlapping cDNAs indicated that these sequences contained an open reading frame with a predicted amino acid sequence of 541 amino acids (SEQ ID NO: 1 and SEQ ID NO: 2). The complete cDNA was termed Mammalian Ena  
25 (Mena). Sequence analysis was carried out using the Genetics Computer Group software package (Devereaux et al., Nuc. Acids Res. 12: 387-395, 1994). The analysis showed significant similarity to Drosophila Ena on the amino acid level. Initial sequence alignments were generated using the PILEUP program and modified using the LINEUP sequence editor

30 The Mena sequence was used to search the GenBank databases at the National Center for Biotechnology Information (Bethesda, MD) using the BLAST program. Two related sequences were identified: VASP (Haffner et al., EMBO J. 14: 19-27, 1995), and

human EST accession #T80305 (obtained from , Washington University-Merck EST Project IMAGE Consortium, LLNL). The EST was used to screen the library as described above. A murine cDNA was isolated and sequenced as previously described in detail. The cDNA (nucleotide sequence and deduced amino acid sequence in SEQ ID NO:7 and SEQ ID NO: 8) was predicted to encode a 393 amino acid protein. Based on  
5 sequence analysis the cDNA was termed Ena-VASP Like (Evl).

Alignment of Mena, Evl, human VASP, and Ena revealed two distinct blocks of similarity flanking a proline-rich core. The consensus sequence is shown in SEQ ID NO: 9. The greatest degree of amino acid identity is in amino terminal 113 amino acid of SEQ  
10 ID NO: 9, which is termed "Ena-VASP homology domain 1" (EVH1). A pair-wise comparison among the 5 sequences throughout the EVH1 domain revealed that Mena and Ena are the most similar of the four Ena-VASP family members. Serine residues aligning to two of the known cyclic nucleotide kinase-dependent phosphorylation sites in VASP (Butt et al., J. Biol. Chem. 269: 14509-14517, 1994) flank the central proline-rich region  
15 of Mena. Evl contains the amino-terminal site only, while Ena lacks both sites. The sequence GPPPPP (SEQ ID NO: 13), which mediates binding of VASP to the actin-monomer sequestering protein profilin (Reinhard et al., EMBO J. 14: 1583-1589, 1995) is present twice in Mena and once in Evl. The carboxy terminal homology domain (EVH2, spanning amino acids 507-733 in the consensus line), contains a putative G-actin binding  
20 sequence, and a conserved charge cluster.

Secondary structure analyses predict that the carboxy terminus of EVH2 is a helical region. Mena also contains a striking five amino-acid repeat region with the consensus LERER (SEQ ID NO: 10), located between the EVH1 domain and the first conserved serine phosphorylation site at amino acid 236 of SEQ ID NO: 2. The extended  
25 helical structure predicted for this repeat may function as a protein-binding interface, or serve to separate the EVH1 domain from the proline-rich core of Mena. Both the EVH2 and the LERER (SEQ ID NO: 10) repeats were predicted to form coiled-coiled domains, structures that are implicated in protein:protein interactions, by the PEPCOIL program, which employs the predictive criteria proposed by Lupas and colleagues (Lupas et al, Science 252: 1162-1164, 1991, which is incorporated herein by reference in its entirety).  
30

The Mena cDNA was used to probe the Jackson backcross hybrid mapping panel (The Jacson Laboratory, Bar Harbor, ME) to determine the chromosomal location of the

*Mena* gene. *Mena* was localized to the mouse chromosome 1a offset 73 which is syntenic to a human chromosomal position 1Q21-23 (Stanier et al., Genomics 26: 473-478, 1995).

### Example 2

#### 5 Mena-Specific Antibodies

To detect *Mena* protein, *Mena*-specific antibodies were developed. DNA fragments encoding amino acids 6-170 of SEQ ID NO: 2 (N-*Mena*) or amino acids 440-537 of SEQ ID NO: 2 (C-*Mena*) were amplified from the *Mena* cDNA using polymerase chain reaction amplification. The fragments were each cloned into pGex2T (Smith and Johnson Gene 67: 31-40, 1988, which is incorporated herein by reference in its entirety) and transformed into a bacterial host to permit the expression of *Mena*-glutathione S-transferase fusion proteins. The fusion proteins were purified on a glutathione-coupled beaded agarose matrix (Glutathione SEPHAROSE, Pharmacia Biotech, Inc., Piscataway, NJ) according to the manufacturer's instructions. Rabbits were immunized and boosted with the *Mena* fusion proteins, and sera collected as described by Harlow and Lane in Antibodies A Laboratory Manual (Cold Spring Harbor, NY, Cold Spring Harbor Press 1988), which is incorporated herein by reference in its entirety. Affinity purified antisera raised against the peptide LKEELIDAIRQELSKSNTA (SEQ ID NO: 11) were produced by Quality Controlled Biochemicals, Inc. (Hopkins, MA). Purified platelet VASP protein was not recognized by any of the *Mena* antibodies tested.

### Example 3

#### Distribution of *Mena*

The distribution of *Mena* protein isoforms during a portion of mouse embryogenesis was determined by Western blot analyses of protein from dissected heads or bodies of embryo-lysates taken from stages E10 to E15 or from lysates of whole E9 embryos. Protein extracts were from cells or dissected embryos were prepared in ice cold RIPA buffer (25 mM Tris (pH 7.5), 150 mM NaCl, 1 % NP40, 0.5% Deoxycholate, 0.1% SDS) + 1 mM PMSF, Aprotinin and 1mM NaVO<sub>4</sub>. Proteins were quantified using the Pierce protein assay kit (Pierce Chemical Company, Rockford, IL).

Immunoprecipitations were performed with 1ml of 1mg/ml of head lysate using 5µl of Anti-N-*Mena* (from rabbit 2188) or 2188 pre-immune sera. Fifty micrograms of protein



were used for Western blotting of total cell lysates. Gel electrophoreses and Western blotting on polyvinyliden fluoride membranes (PVDF, Millipore, Bedford, MA) were performed as described by Harlow and Lane (ibid.) and according to the manufacturer's instructions. Signals were visualized using chemiluminescence (Dupont Co. (NEN Life Science Products), Wilmington, DE).

Western analysis of the dissected embryo lysates showed two bands migrating at 80 and 88 kD in all of the lysates, while a 140 kD signal was enriched in head fractions and increased in intensity from E10-E15, an interval of development during which there is rapid neurite outgrowth. In adult tissues, the 140 kD form was found only in brain extracts and not in muscle, lung, kidney, heart, liver or thymus. In addition, an approximately 60 kD Mena protein was detected in certain hematopoietic cells.

The 140 kD band was also enriched during the course of retinoic acid-induced differentiation of the P19 embryonic carcinomal stem cells into neurons (Rudnicki and McBurney, Cell Culture Methods and Induction of Differentiation of Embryonal Carcinoma Cell Lines. In Teratocarcinomas and Embryonic Stem Cells: A Practical Approach, E. Robertson, ed., Oxford, England, pp. 19-47, 1987; which is incorporated herein by reference in its entirety). Anti-Mena Western blot analyses of lysates from P19 embryonic carcinomal cells at 0,3,5, and 7 days after treatment with retinoic acid demonstrated that the 140 kD form of Mena was induced during the differentiation process. Similar results were observed using antisera directed against the amino terminus, carboxy terminus, or an affinity-purified anti-peptide antibody. Immunofluorescent staining of differentiated P19 cells with Mena-specific antibodies shows that Mena protein is concentrated in the growth cone of the neurite. Mena immunoreactivity was also observed along the length of the neurite and in the cell body.

The mobility of the 80 kD and 140 kD Mena isoforms was slower than that predicted by their sequence (60 kD and 83 kD respectively), perhaps due to structural effects of their large proline content. The Mena cDNA was translated *in vitro* to produce <sup>35</sup>S-labeled Mena protein using the TNT coupled transcription/translation system (Promega Corp, Madison, CA). The translation products were subjected to gel electrophoresis, and the gels were fixed and treated with Amplify (Amersham, Arlington Heights, IL). The fixed gels were dried and quantified using a phosphorimager (Molecular Dynamics, Sunnyvale, CA). Translation of the Mena cDNA gave rise to a protein that co-

migrates with the 80 kD band, while expression of the neural Mena cDNA (Example 4) in fibroblasts produced a signal at 140 kD in addition to the endogenous doublet at 80 kD. These data indicate that the 80 kD signal is a broadly expressed form of Mena, while the 140 kD signal is a Mena isoform enriched in, or specific to neural cell types and produced by alternative splicing. The 88 kD signal is immunoreactive with all anti-Mena antibodies tested, and may represent another splice variant, or a post-translationally modified form of Mena.

#### Example 4

##### 10 Cloning of Neural Mena cDNAs

To clone the larger neural-enriched proteins identified as being immunologically related to Mena a mouse brain cDNA library with the Mena cDNA. The Mena cDNA was radiolabeled and used to screen a mouse brain library (Stratagene Cloning Systems, La Jolla, CA) using the methods described above. Complementary DNAs combinations of three alternately included exons spliced into the original sequence were isolated. Neural Mena<sup>\*</sup>, contained an exon that introduces 244 amino acids (corresponding to amino acid 239 through amino acid 482 of SEQ ID NO: 4) between amino acids 238 and 239 of (SEQ ID NO: 2). The nucleotide sequence and deduced amino acid sequences of neural Mena are shown in (SEQ ID NO: 3 and SEQ ID NO:4). Two other isoforms, neural Mena<sup>\*\*</sup> and neural Mena<sup>\*\*\*</sup> contained the exon insertion described for Neural Mena<sup>\*</sup> and either a exon insertion between amino acids 116 and 117 of SEQ ID NO: 2. The deduced amino acid sequences of neural Mena<sup>\*\*</sup> and neural Mena<sup>\*\*\*</sup> are shown in SEQ ID NO: 5 and SEQ ID NO:6, respectively.

25

#### Example 5

##### Phosphorylation of Mena

The presence of potential phosphorylation sites in the deduced amino acid sequence of Mena and the phosphorylation that has been demonstrated on VASP and Ena suggests that Mena is phosphorylated. The phosphorylation status of Mena was determined by immunoprecipitation. RIPA lysates from E12 embryonic heads were

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immunoprecipitated using anti-N terminal Mena antibodies or pre-immune sera . The precipitates were analyzed by Western blotting as described above with the 4G10 anti-phosphotyrosine monoclonal antibody. Mena immunoprecipitates from E12 head lysates contained an anti-phosphotyrosine reactive signal that co-migrates with the 140 kD form.

5 The 80 and 88 kD forms contained no detectable phosphotyrosine.

Mena expression was examined in the rat embryo line Rat2 (ATCC CRL 1764). The cells were grown in Dulbecco's Modified Eagle's Medium (DMEM; Life Technologies (GIBCO/BRL), Gaithersburg, MD) supplemented with 10% FCS. In Rat2 cells, Mena migrates as an 80 kD doublet. Treatment of Mena protein with purified  
10 protein kinase A (New England Biolabs, Beverly, MA) according the manufacturer's instructions caused a quantitative conversion of the 80 kD form of Mena to the slower migrating form of the doublet.

The Mena cDNA was translated *in vitro* and labeled with <sup>35</sup>S-methionine as described previously. The translation product migrated as an 80 kD doublet. Addition of  
15 protein kinase A shifted the mobility of the lower band to that of the upper, indicating that this doublet was caused by partial serine phosphorylation in the lysate.

### Example 6

#### Subcellular Localization of Mena

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The subcellular distribution of Mena in non-neural cell types was determined by immunofluorescence. Rat2 cells were grown in DMEM (Life Technologies (GIBCO/BRL), Gaithersburg, MD) supplemented with 10% FCS on glass coverslips coated with 5 µg/cm<sup>2</sup> fibronectin (Sigma Biosciences, St. Louis, MO). Cells were fixed  
25 with either 3% or ice-cold 4% paraformaldehyde in phosphate buffered saline (PBS) for 10 minutes. The fixed cells were permeabilized with 0.2% (v/v) Triton X-100 in PBS and stained as described (Harlow and Lane, *ibid.*). Mena-specific antisera was used at dilution of 1:400. Fluorescein (FITC) and Texas Red secondary antibody conjugates were purchased from Jackson ImmunoResearch Laboratories, Inc., West Grove, PA) and used at  
30 a dilution of 1:100. Phosphotyrosine and neurofilaments detected using mab4G10 (Upstate Biotechnology, Inc., Lake Placid, NY), and mab 2H3D12 (obtained from Tom Jessell, Columbia University, New York, NY). Bodipy phalloidin (Molecular Probes Inc.,

Eugene, OR) was used to stain F-actin, DAPI (Sigma, St. Louis, MO) was used to stain nuclei, and Vectashield mounting media (Vector Labs, Burlingame, CA) were used to in the preparation of the images. Three dimensional microscopic images were captured and processed using a Deltavision microscope and software (Applied Precision Inc., Mercer  
5 Island, WA).

Subcellular distribution of Mena in Rat2 cells was observed in a subdomain of Focal adhesion structures. Phosphotyrosine appeared distal to Mena, followed by a region of overlap, and a proximal region that contains Mena. Note that, unlike VASP, high levels of Mena are not observed along the length of actin stress fibers. The staining was specific  
10 for Mena, as signal was not observed in cells stained with preimmune sera, or in macrophages which contain VASP, but not Mena. Similar Mena staining was observed with both anti-N-Mena, and anti-C-Mena antibodies. The distribution of Mena was compared to phosphotyrosine, a marker for focal adhesions (Maher et al., Proc. Natl. Acad. Sci. USA 82, 6576-6580 1985). Mena was restricted to the proximal portions of  
15 the phosphotyrosine domain in most focal contacts, at the ends of F-actin stress fibers. Therefore, Mena distribution overlaps with molecules that are receiving extracellular matrix-induced signals and with regions of microfilament assembly.

#### Example 7

##### 20 EHV1 domain binding

To investigate whether the highly conserved EVH1 domain mediates an interaction with zyxin or vinculin, molecules that may recruit Mena to focal adhesions in fibroblasts or related structures in other cell types), the EVH1 domain was used to purify proteins from  
25 embryo cell lysates. N-Mena-Gst, the Gst-fusion protein containing amino acids 6-170 of Mena (described in Example 2) encompasses the EVH1 domain. Five micrograms of N-Mena-Gst or Gst alone was immobilized on a glutathione-coupled beaded agarose matrix (Glutathione SEPHAROSE, Pharmacia Biotech, Inc., Piscataway, NJ) according to the manufacturer's instructions. The N-Mena matrix was mixed with 1ml of 1mg/ml of RIPA  
30 lysates of E12 heads, or human erythrocytic leukemia cells (HEL) (described above) and incubated overnight at 4°C. Samples were washed three times in RIPA, and bound proteins analyzed by Western blot analysis with antibodies to zyxin (obtained from Dr.

Mary Beckerle University of Utah), vinculin or the Ack kinase (Santa Cruz Biotechnology Inc., Santa Cruz, CA), which contains a similar proline-rich motif. The antibodies were used at a 1:100 dilution. The N-Mena matrix retained more than 50% of the total endogenous zyxin, and detectable amounts of vinculin. Ack was not recovered detectably, indicating that the motif in Ack lacks some feature critical for binding *in vivo*, or that the sequence is not accessible. These results indicate that N-Mena is capable of binding to zyxin and vinculin.

To test the ability of Mena to bind ActA, PtK<sub>2</sub>, potoroo kidney epithelial cells, (ATCC CCL 56) were seeded in Modified Essential Medium (MEM; Life Technologies (GIBCO/BRL), Gaithersburg, MD) supplemented with 10% FCS, glutamine and non-essential amino acids to semi confluency onto CELLocate coverslips (Eppendorf, Hamburg, Germany) two days prior to microinjection. Purified Gst-N terminal Mena fusion protein was microinjected into the cytoplasm of the cells and GST alone served as a control. After injection, the cells were returned to the incubator for 15 to 30 minutes before fixation.

For the detection of microinjected proteins directed to subcellular structures, an extraction of the cytoplasm before fixation was performed by washing the cells with MES-buffer (0.1 M MES, 4 % PEG 6000 (w/v), 1 mM MgCl<sub>2</sub> (pH 7.6)) twice followed by a two minute incubation with MES-buffer with 0.2% Triton X-100. After another wash with MES-buffer, cells were fixed with paraformaldehyde, and then incubated 30 minutes each with primary and fluorescently labeled secondary antibodies and phalloidin. Microinjected Gst-N terminal Mena fusion protein was detected using polyclonal anti-GST antibodies. Fluorescence photomicroscopy was carried out on a Zeiss Axiophot with appropriate filter sets for epifluorescence detection of FITC and rhodamine signals. The microinjection of N-Mena-Gst fusion protein into PtK<sub>2</sub> cells demonstrated that the N-Mena sequences directed the fusion protein to focal adhesions. When Gst alone was injected, diffuse signal was observed throughout the cell.

A peptide corresponding to amino acids 293-312 of the ActA sequence (SEPSSFEPPTDEELRLA, SEQ ID NO: 12) was also injected into PtK<sub>2</sub> cells. The ActA peptide (SEQ ID NO. 12) was first coupled to ovalbumin as described previously (Pistor et al., Curr. Biol. 5: 517-525, 1995; which is incorporated herein by reference in its entirety), and the conjugate was microinjected along with rhodamine-coupled BSA as a

marker protein. The cells were then returned to the incubator for 15 to 30 minutes before fixation.

Microinjection of the ActA peptide (SEQ ID NO.12) was resulted in the depletion of the endogenous Mena protein from focal contacts in the injected cells. In contrast,  
5 Mena distribution was not affected by injection of a peptide corresponding to an unrelated portion of ActA. However, the distribution of vinculin was not altered by the injected peptide, confirming that the effect is specific. Taken together, these data indicate that the N-terminal portion of Mena, which contains the EVH1 domain, can direct its proper  
10 localization to focal contacts via direct protein:protein interactions with zyxin, vinculin or other focal adhesion proteins containing an ActA-like motif. These proteins contain the sequence FPPPP (SEQ ID NO: 17) suggesting that this motif may comprise the core recognition site in EVH1 ligands.

#### Example 8

##### 15 Mena Modulates F-actin Dynamics

To examine whether increased concentration of Mena protein might stimulate actin nucleation and polymerization, a retroviral vector was used to drive increased levels, or ectopic expression of the different Mena isoforms in Rat2 cells. Rat2 cells were grown  
20 under conditions described previously. Retroviruses were constructed by inserting full length Mena cDNAs (Mena, neural Mena, Isoform 1 or Isoform 2) into the pBABE vector (Morgenstern and Land, Nuc. Acids Res. 18: 3587-3596, 1990, which is incorporated herein by reference in its entirety), packaged and used to infect fibroblasts as described Morgenstern and Land (ibid.).

25 Cells were immunostained to determine the distribution of Mena and F-actin three days after infection with the parental virus or viruses programmed to express the various Mena isoforms. Expression of the 80 kD form of Mena caused the formation of localized clusters of Mena and F-actin. More dramatic results were observed when any of the three neural variants of Mena were used.

30 The over-expression of neural Mena was particularly dramatic. As expected, individual cells in the experimental population expressed varying degrees of neural Mena as judged by fluorescence intensity. Similar increases in Mena immunofluorescence

intensity across the population were observed with the 80 kD form, or any of the three neural Mena variants. Western analysis indicated that, over the whole population, the cumulative amount of ectopic neural Mena protein produced was roughly equivalent to the endogenous content of the 80 kD Mena isoform. About 25% of cells had detectable levels of Mena immunoreactivity outside focal contacts. These cells often contained concentrated pools of immunoreactivity that overlapped with dense accumulations of F-actin. Projection of a three dimensional rendering of the image at a 45° angle indicated that the Mena-actin structures were protuberances from the cell surface. Scanning electron microscopy confirmed the presence of cell-surface projections on a subset of cells from a similarly infected pool, but not in the corresponding control. An optical section taken at the plane of cell-substratum contact showed a relatively normal distribution of Mena, mainly in focal contacts and at the cell periphery, and F-actin, mainly in typical stress fibers. An optical section taken 3.8 µm above the substratum contact indicated the Mena-induced projections extend above the top of the nuclei. Comparison of the Mena and F-actin staining at this level indicated that Mena is distributed at the periphery of the F-actin, potentially at the site of F-actin polymerization and nucleation in these projections. These data indicate that, when ectopically expressed in fibroblasts, the neural form of Mena can direct the formation of cell surface projections.

#### Example 9

##### Mena Interacts with Profilin and SH3

The ability of Mena to interact with SH3 and profilin binding was determined by using assays were described by Reinhard et al. (ibid., 1995) and Weng et al. (J. Biol. Chem. 268: 14956-14963, 1993), which are incorporated herein by reference in their entirety). Mena protein was labeled with <sup>35</sup>S-methionine by *in vitro* using the TNT coupled transcription/translation system (Promega Corp, Madison, CA) according to the manufacturer's instruction.

Briefly, profilin was coupled to a NHS-activated agarose matrix (NHS-activated HiTrap-column, Pharmacia Biotech, Inc., Piscataway, NJ) following the manufacturer's instructions. Chromatography steps were carried out at 4°C. Radiolabeled Mena protein was loaded onto the column in the presence or absence of 1 mg/ml GPPPPP (SEQ ID NO:

13). Proteins were eluted from the column with buffer B (50 mM Tris-HCl (pH 7.2), 1 mM DTE, 5 mM MgCl<sub>2</sub>, 150 mM NaCl, 0.1% BSA) with 5 mg/ml poly-L-proline (1-10 kD, Sigma, St. Louis, MO). The eluates were analyzed by SDS-PAGE and autoradiography. Autoradiography demonstrated that 83% of the input Mena was retained on the profilin-SEPHAROSE column as determined by phosphorimager analysis of the gel. Equal binding of the phospho- and dephospho forms of Mena was observed. In the presence of the competitor peptide, the amount of Mena retained was reduced to 13%.

Mena-profilin binding was also assessed by incubating  $5 \times 10^{15}$  M of Mena with increasing concentrations of profilin to determine the % of Mena bound. In this assay, the profilin-SEPHAROSE matrix was diluted with Sepharose to create columns bound with known, increasing profilin concentrations. The  $5 \times 10^{15}$  M of *in vitro* translated, radiolabeled Mena was mixed with profilin-Sepharose matrix and unbound Mena was washed from the column. The bound Mena was quantified by scintillation analysis. This analysis demonstrated that the Mena binding is saturable.

Mena binding was assayed for Gst-AbiSH3, GstScrSH3 (described by Gertler et al., *ibid.*, 1995; which is incorporated herein by reference in its entirety). The Gst fusion proteins were each bound to glutathione-SEPHAROSE as described previously. The SH3-SEPHAROSE matrix was then gel electrophoresis and autoradiography. Gst alone was used as a control, and as expected, no binding to Gst was observed. The AbiSH3 retained 21% and 14% of the input dephospho-, or Phosphorylated input Mena, respectively. The SrcSH3 retained 8% and 3% of the dephospho-, or phosphorylated Mena, respectively. In both cases, the dephosphorylated form of Mena was more efficiently purified from the lysate.

The Gst-SH3 fusion proteins were also used to purify Mena from RIPA head lysates. The Gst-fusion proteins were each bound to the glutathione-SEPHAROSE matrix as described above. RIPA head lysates were added to the matrix. The matrix was washed, and the bound protein was eluted and analyzed. Using this method both the broadly distributed and neural Mena forms were purified. These results indicate that a subset of interactions mediated by the proline-rich core of Mena could be modulated by serine-threonine phosphorylation.



### Example 10

#### Mena Localization in *Listeria* Infection

To determine if Mena is involved in the microfilament assembly required for *Listeria* motility, the distribution of Mena was examined in infected cells. *L. monocytogenes* serotype 1/2a EGD were grown in brain-heart infusion (BHI) broth (DIFCO Laboratories, Inc., Detroit, MI) at 37°C with aeration. For infection experiments PtK<sub>2</sub> cells were grown on coverslips, and bacteria from an overnight culture were added directly to the culture medium at a dilution of 1:200. After 1-2 hours the plates were extensively washed with fresh medium containing 25 µg/ml gentamicin to kill extracellular bacteria. After further incubation for 2-3 hours the coverslips were washed and processed for immunofluorescence as described above. Immunofluorescence demonstrated that Mena is depleted from focal contacts and recruited to the bacterial surface upon infection with *Listeria monocytogenes*. Analogous to its appearance in focal adhesions, Mena distribution overlaps with the pole of the bacterium associated with the formation of new F-actin. The Gst-N-Mena was microinjected into PtK<sub>2</sub> cells. The cells were treated as described above, except that after infection, the cells were allowed to recover for at least two hours. After infection of the injected cells with *Listeria*, the exogenous Mena protein was recruited to the surface of the bacterium. These results implicate the EVH1 domain of Mena and VASP in the ActA-dependent redistribution of these proteins to the bacterial surface.

### Example 11

#### Construction of Knock out Mice and Immortomouse Mena<sup>-</sup> Mice

Knock-out mice in which the murine Mena coding sequence was replaced with the β-galactosidase gene and the neomycin resistance gene (neo) were generated i) to assess the consequences of eliminating the murine Mena protein during mouse development ii) to permit examination of the expression pattern of *Mena* in embryonic mice iii) to generate Mena<sup>-</sup> cell lines and iv) to cross the mice with mice carrying onco-genes to study the effects of such double mutants. Genomic *Mena* sequences used for these knock-out mice were obtained from the 129/Sv mice so that the homologous recombination could take place in a congenic background in 129/Sv mouse embryonic stem cells. Mena genomic clones

were isolated from a genomic library prepared from 129/Sv mice (Zhuang et al., Cell 79: 875-884, 1994; which is incorporated herein by reference in its entirety) using a random-primed Mena cDNA probe. Plasmid pSA $\beta$ Geolox2DTA contains the  $\beta$ -galactosidase/neomycin resistance gene fusion ( $\beta$ Geo) and the *Diphtheria* toxin gene under the control of the PGK promoter in a pBLUESCRIPT (Stratagene Cloning Systems, La Jolla, CA) vector backbone was used to create the targeting construct. A 10 kb 5' Mena genomic fragment, the 4 kb cytoplasmic  $\beta$ Geo gene and the 1 kb fragment containing the genomic 3' untranslated sequence of Mena was inserted 5' of the Diphtheria toxin expression cassette in the pSA $\beta$ Geolox2DTA vector backbone.

The targeting construct was linearized at a unique restriction site in the vector backbone and was transfected by electroporation into mouse embryonic stem (ES) cells. A 129/Sv derived ES cell line, AK-7 described by Zhuang et al. (ibid.) was used for electroporation. These ES cells were routinely cultured on mitomycin C-treated (Sigma) SNL 76/7 cells (feeder cells) as described by McMahon and Bradley (Cell 62: 1073-1085, 1990; which is incorporated herein by reference in its entirety) in culture medium containing high glucose DMEM supplemented with 15% fetal bovine serum (Hyclone) and 0.1  $\mu$ M (micromolar)  $\beta$ -mercaptoethanol. To prepare the targeting construct for transfection, 25 g (micrograms) of the targeting construct was linearized by digestion with Not I, phenol-chloroform extracted, and ethanol precipitated. The linearized vector was then electroporated into  $1-2 \times 10^7$  AK-7 (ES) cells. The electroporated cells were seeded onto three 10-cm plates with one plate receiving 50% of the electroporated cells and the remaining two plates each receiving 25% of the electroporated cells. After 24 hours, G418 was added to each of the plates to a final concentration of 300  $\mu$ g/ml (micrograms per milliliter). The culture medium for each plate was changed every day for the first few days, and then changed as needed after selection had occurred. After 10 days of selection, a portion of each colony was picked microscopically with a drawn micropipette, and was directly analyzed by PCR as described by Joyner et al. (Nature 338: 153-156, 1989; which is incorporated herein by reference in its entirety). Briefly, PCR amplification was performed as described (Kogan et al., New England J. Med. 317: 985-990, 1987; which is incorporated herein by reference in its entirety) using 40 cycles of 93°C for 30 seconds, 57°C for 30 seconds, and 65°C for 3 minutes. To detect the wild-type allele, primers MF

and MR (SEQ ID NOS:14 and 15, respectively) were used in the PCR reaction, to detect the mutant *Mena* allele, primers BPAF and MR (SEQ ID NOS: 16 and 15, respectively) were used in the PCR reaction. Positive colonies, identified by PCR, were subcloned into 4-well plates, expanded into 60 mm plates and frozen into 2-3 ampules. Among the clones  
5 that were selected for both G418-resistance (positive selection for *neo* gene expression) 95% of the population contained correctly targeted integration of the vector into the murine *Mena* locus.

To generate chimeric mice, each positive clone was thawed and passaged once on feeder cells. The transfected cells were trypsinized into single cells, and blastocysts  
10 obtained from C57BL/6J mice were injected with approximately 15 cells. The injected blastocysts were then implanted into pseudopregnant mice (C57BL/6J x CBA). Six male chimeras arose from the injected blastocysts. All of the male chimeras gave germ-line transmission at a high rate as determined by the frequency of agouti coat color transmission to their offspring (F1) in a cross with C57BL/6J female mice. Since 50% of  
15 the agouti coat color offspring (F1) should represent heterozygous mutants, their genotypes were determined by Southern blot analysis. Briefly, genomic DNA prepared from tail biopsies was digested with Eco R1 and probed with the a 3 kb 5' genomic sequence flanking the targeting construct. This probe detects a 16 kb fragment from the wild-type allele and a 10 kb fragment from the mutant allele. Therefore, a Southern  
20 analysis would show a single 16 kb band for a wild-type mouse, 16 kb and 10 kb fragments for a heterozygous mouse, and a single 10 kb band for a homozygous mutant mouse. The resulting offspring (F1), heterozygous (+/-) mice, were mated with sibling heterozygous mice to give rise to the homozygous (-/-) mutant mice.

To study *Mena* expression patterns in embryonic mice, chimeric mice or F1  
25 heterozygous progeny from the chimera x C57B/6J mating were crossed with C57B/6J. Litters resulting from these crosses were harvested from pregnant females and stained for  $\beta$ -galactosidase activity. The embryos were dissected away from all the extra-embryonic tissue and the yolk sac was reserved for DNA analysis. The embryos were fixed for one hour in a Fix solution containing (0.1 M phosphate buffer containing 0.2% glutaraldehyde,  
30 2% formaldehyde, 5 mM EGTA (pH 7.3), 2 mM MgCl<sub>2</sub>). The fixing solution was removed by three thirty-minute rinses with rinse solution (0.1 M phosphate buffer (pH 7.3) containing 2 mM MgCl<sub>2</sub>, 0.1% sodium deoxycholate, 0.2% NP-40). The fixed embryos

were stained overnight in the dark in rinse solution containing 1 mg/ml X-gal, 5 mM sodium ferricyanide, 5 mM sodium ferrocyanide. After staining, the embryos were rinsed with PBS and stored in the Fix solution before preparation for examination. Examination of stained tissue from fetal and postnatal mice heterozygous for the mutation demonstrated

5 Mena expression pattern in the nervous system, somites, muscle tissue, neural crest cells and in the gut.

To generate mice from which Mena<sup>-</sup> cell lines may be derived, a heterozygous Mena knock-out mouse were crossed with an IMMORTOMOUSE (Charles River Laboratories, Wilmington, MA). IMMORTOMOUSE is a mouse carrying a H-2Kb-tsA58

10 SV40 large T antigen transgene. The progeny of the cross were subjected to PCR analysis as generally described above to identify progeny carrying the transgene and are heterozygous for the *Mena* knock out gene. The progeny carrying both the transgene and the *Mena* knock out gene were back-crossed to the Mena<sup>-</sup> heterozygotes. The progeny of the back-cross were subjected to PCR analysis to identify homozygous Mena<sup>-</sup> progeny

15 carrying the transgene. Cells from the resulting mice may be immortalized by culturing the cells at 33°C in the presence of interferon.

Those with ordinary skill in the art will appreciate that other embodiments and variations of the invention are possible which employ the same inventive concepts described above. Therefore, the invention is not to be limited except by the above

20 description, but is to be determined in scope by the claims which follow.

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: Gertler, Frank B  
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Niebuhr, Kirsten  
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  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: US
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
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## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2172 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Mus musculus
- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: Mena
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 140..1765
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGCGTCCGCC TCCCCGCTG AGAAGAGACC CTCCGCTCGG CGGCTCCCGC GCCGGGGAAG	120
CCTCGGCGCC GCCGGCACC ATG AGT GAA CAG AGT ATC TGT CAG GCA AGA GCT	172
Met Ser Glu Gln Ser Ile Cys Gln Ala Arg Ala	
1 5 10	
GCT GTG ATG GTC TAT GAT GAT GCC AAT AAG AAG TGG GTG CCA GCT GGT	220
Ala Val Met Val Tyr Asp Asp Ala Asn Lys Lys Trp Val Pro Ala Gly	
15 20 25	
GGC TCA ACT GGG TTC AGC AGA GTA CAT ATA TAT CAC CAT ACA GGC AAC	268
Gly Ser Thr Gly Phe Ser Arg Val His Ile Tyr His His Thr Gly Asn	
30 35 40	
AAC ACA TTC AGA GTT GTG GGC AGA AAG ATT CAA GAC CAT CAG GTT GTG	316
Asn Thr Phe Arg Val Val Gly Arg Lys Ile Gln Asp His Gln Val Val	
45 50 55	
ATA AAC TGT GCC ATT CCT AAA GGG CTG AAG TAC AAT CAA GCT ACA CAG	364
Ile Asn Cys Ala Ile Pro Lys Gly Leu Lys Tyr Asn Gln Ala Thr Gln	
60 65 70 75	
ACT TTC CAC CAA TGG AGG GAT GCT AGA CAG GTG TAT GGT CTC AAC TTT	412
Thr Phe His Gln Trp Arg Asp Ala Arg Gln Val Tyr Gly Leu Asn Phe	
80 85 90	
GGC AGC AAA GAG GAT GCC AAT GTC TTC GCA AGT GCC ATG ATG CAT GCC	460
Gly Ser Lys Glu Asp Ala Asn Val Phe Ala Ser Ala Met Met His Ala	
95 100 105	
TTA GAA GTG TTA AAT TCA CAG GAA GCA GGG CCA ACA TTG CCT AGA CAA	508
Leu Glu Val Leu Asn Ser Gln Glu Ala Gly Pro Thr Leu Pro Arg Gln	
110 115 120	
AAT TCA CAG CTA CCT GCT CAA GTT CAA AAT GGC CCA TCC CAA GAA GAG	556
Asn Ser Gln Leu Pro Ala Gln Val Gln Asn Gly Pro Ser Gln Glu Glu	
125 130 135	
CTG GAA ATC CAG AGA AGG CAA CTG CAA GAA CAG CAG CGA CAG AAG GAA	604
Leu Glu Ile Gln Arg Arg Gln Leu Gln Glu Gln Gln Arg Gln Lys Glu	
140 145 150 155	
CTG GAG AGG GAA AGA ATG GAG AGG GAA AGG TTG GAG AGA GAA CGA CTA	652
Leu Glu Arg Glu Arg Met Glu Arg Glu Arg Leu Glu Arg Glu Arg Leu	
160 165 170	
GAA CGA GAG AGG CTA GAG AGG GAG CGC CTG GAA CAA GAG CAG CTG GAG	700
Glu Arg Glu Arg Leu Glu Arg Glu Arg Leu Glu Gln Glu Gln Leu Glu	
175 180 185	
CGG CAG CGG CAG GAA AGG GAG CAC GTG GAG CGG CTG GAG AGG GAG AGG	748
Arg Gln Arg Gln Glu Arg Glu His Val Glu Arg Leu Glu Arg Glu Arg	
190 195 200	
CTG GAG CGC CTG GAG CGA GAG AGG CAG GAG CGG GAG CGA GAG CGC CTG	796
Leu Glu Arg Leu Glu Arg Glu Arg Gln Glu Arg Glu Arg Glu Arg Leu	
205 210 215	
GAG CAG CTG GAG CGG GAG CAA GTG GAG TGG GAG CGA GAG CGC AGA ATG	844
Glu Gln Leu Glu Arg Glu Gln Val Glu Trp Glu Arg Glu Arg Arg Met	
220 225 230 235	
TCC AAT GCT GCT GCC CCT GCC TCT GCG GAG ACC CCT CTA AAT CCT GAG	892
Ser Asn Ala Ala Ala Pro Ala Ser Ala Glu Thr Pro Leu Asn Pro Glu	
240 245 250	

CTG	GGA	GAC	TCC	TCT	GCT	TCC	GAG	CCA	GGC	TTG	CAG	GCA	GCC	TCT	CAG	940
Leu	Gly	Asp	Ser	Ser	Ala	Ser	Glu	Pro	Gly	Leu	Gln	Ala	Ala	Ser	Gln	
			255					260					265			
CCG	GCC	GAG	TCG	CCA	ACC	CCA	CAG	GGC	CTT	GTC	TTG	GGA	CCA	CCT	GCA	988
Pro	Ala	Glu	Ser	Pro	Thr	Pro	Gln	Gly	Leu	Val	Leu	Gly	Pro	Pro	Ala	
		270					275					280				
CCT	CCG	CCA	CCA	CCC	CCT	CTC	CCA	TCA	GGC	CCT	GCC	TAC	GCC	TCA	GCA	1036
Pro	Pro	Pro	Pro	Pro	Pro	Leu	Pro	Ser	Gly	Pro	Ala	Tyr	Ala	Ser	Ala	
		285				290					295					
CTT	CCT	CCT	CCC	CCA	GGA	CCC	CCT	CCA	CCA	CCT	CCA	CTG	CCA	TCC	ACT	1084
Leu	Pro	Pro	Pro	Pro	Gly	Pro	Pro	Pro	Pro	Pro	Pro	Leu	Pro	Ser	Thr	
300					305					310					315	
GGT	CCT	CCT	CCT	CCA	CCC	CCT	CCA	CCA	CCC	CCT	CTT	CCT	AAT	CAA	GCT	1132
Gly	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Leu	Pro	Asn	Gln	Ala	
				320					325					330		
CCT	CCC	CCT	CCT	CCC	CCA	CCT	CCT	GCC	CCT	CCC	CTC	CCC	GCA	TCT	GGA	1180
Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Ala	Pro	Pro	Leu	Pro	Ala	Ser	Gly	
				335				340					345			
ATT	TTC	TCT	GGA	TCC	ACG	TCA	GAA	GAC	AAT	CGC	CCT	TTA	ACT	GGA	CTT	1228
Ile	Phe	Ser	Gly	Ser	Thr	Ser	Glu	Asp	Asn	Arg	Pro	Leu	Thr	Gly	Leu	
		350					355					360				
GCA	GCT	GCA	ATT	GCG	GGA	GCA	AAA	CTT	AGG	AAA	GTG	TCC	CGG	GTG	GAG	1276
Ala	Ala	Ala	Ile	Ala	Gly	Ala	Lys	Leu	Arg	Lys	Val	Ser	Arg	Val	Glu	
		365				370					375					
GAT	GGC	TCT	TTC	CCA	GGT	GGA	GGG	AAT	ACT	GGG	AGT	GTG	AGC	TTG	GCC	1324
Asp	Gly	Ser	Phe	Pro	Gly	Gly	Gly	Asn	Thr	Gly	Ser	Val	Ser	Leu	Ala	
380					385					390					395	
TCA	TCC	AAA	GCA	GAC	GCT	GGG	CGT	GGG	AAT	GGA	CCT	CTT	CCT	CTA	GGG	1372
Ser	Ser	Lys	Ala	Asp	Ala	Gly	Arg	Gly	Asn	Gly	Pro	Leu	Pro	Leu	Gly	
				400					405					410		
GGT	AGT	GGC	TTA	ATG	GAA	GAA	ATG	AGT	GCC	CTG	CTG	GCC	AGG	AGG	AGA	1420
Gly	Ser	Gly	Leu	Met	Glu	Glu	Met	Ser	Ala	Leu	Leu	Ala	Arg	Arg	Arg	
			415					420					425			
AGA	ATT	GCT	GAG	AAG	GGA	TCA	ACA	ATA	GAA	ACA	GAA	CAA	AAG	GAA	GAC	1468
Arg	Ile	Ala	Glu	Lys	Gly	Ser	Thr	Ile	Glu	Thr	Glu	Gln	Lys	Glu	Asp	
		430					435					440				
AGA	AAT	GAA	GAT	GCA	GAG	CCT	ATA	ACT	GCT	AAG	GCC	CCA	TCA	ACA	AGT	1516
Arg	Asn	Glu	Asp	Ala	Glu	Pro	Ile	Thr	Ala	Lys	Ala	Pro	Ser	Thr	Ser	
		445				450					455					
ACA	CCT	GAA	CCA	ACC	AGA	AAA	CCT	TGG	GAA	AGA	ACA	AAC	ACA	ATG	AAC	1564
Thr	Pro	Glu	Pro	Thr	Arg	Lys	Pro	Trp	Glu	Arg	Thr	Asn	Thr	Met	Asn	
460					465					470					475	
GGC	AGT	AAG	TCA	CCT	GTC	ATC	TCC	AGA	CCC	AAA	TCC	ACA	CCT	TCA	TCA	1612
Gly	Ser	Lys	Ser	Pro	Val	Ile	Ser	Arg	Pro	Lys	Ser	Thr	Pro	Ser	Ser	
				480					485					490		
CAG	CCA	AGT	GCC	AAT	GGA	GTC	CAG	ACA	GAA	GGC	CTT	GAC	TAT	GAC	AGG	1660
Gln	Pro	Ser	Ala	Asn	Gly	Val	Gln	Thr	Glu	Gly	Leu	Asp	Tyr	Asp	Arg	
			495				500						505			
CTG	AAG	CAG	GAC	ATT	TTA	GAT	GAG	ATG	AGA	AAA	GAG	CTG	GCA	AAG	CTG	1708
Leu	Lys	Gln	Asp	Ile	Leu	Asp	Glu	Met	Arg	Lys	Glu	Leu	Ala	Lys	Leu	
		510					515					520				

AAG GAG GAG CTT ATT GAC GCA ATC AGG CAG GAG CTG AGC AAG TCG AAC	1756
Lys Glu Glu Leu Ile Asp Ala Ile Arg Gln Glu Leu Ser Lys Ser Asn	
525 530 535	
ACT GCA TAAAGAAGCA AACTACGGAG GGGCAGGACT TGAATCTGGA GAAAACAAAA	1812
Thr Ala	
540	
ATTCCTACAA ACAACTCTTA ACCCCCAAAC TTTTAAGCTG TAAGAAGAAA ATGGATACAC	1872
AGTCAGGAGG GAAGCCGTCA ACCTCTGAAA GCCTCAGACA GTGACTCTGG CGATCAGCTG	1932
TCCCCTCAGT GTGCTGCTTT ATTCTGTCTG ACCTTTACCA CAGGATGGAG AATGATATTG	1992
GAGTTCCCTT AGCAGTACTA AACCCGTCAG GCAAGATCAC CGTGCATTGA AATATTTTCA	2052
TGTCTAGATG AGTCTGCACG TTTTCCATAA TCCATTGCTA AAATAAAGAC GAGAAAGGGT	2112
AAATCTCGAG GAATTCATAA TTTTTCCTC CAGATCCTCT AGAGTCCTGT TTCCTGTGTG	2172

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ser Glu Gln Ser Ile Cys Gln Ala Arg Ala Ala Val Met Val Tyr	
1 5 10 15	
Asp Asp Ala Asn Lys Lys Trp Val Pro Ala Gly Gly Ser Thr Gly Phe	
20 25 30	
Ser Arg Val His Ile Tyr His His Thr Gly Asn Asn Thr Phe Arg Val	
35 40 45	
Val Gly Arg Lys Ile Gln Asp His Gln Val Val Ile Asn Cys Ala Ile	
50 55 60	
Pro Lys Gly Leu Lys Tyr Asn Gln Ala Thr Gln Thr Phe His Gln Trp	
65 70 75 80	
Arg Asp Ala Arg Gln Val Tyr Gly Leu Asn Phe Gly Ser Lys Glu Asp	
85 90 95	
Ala Asn Val Phe Ala Ser Ala Met Met His Ala Leu Glu Val Leu Asn	
100 105 110	
Ser Gln Glu Ala Gly Pro Thr Leu Pro Arg Gln Asn Ser Gln Leu Pro	
115 120 125	
Ala Gln Val Gln Asn Gly Pro Ser Gln Glu Glu Leu Glu Ile Gln Arg	
130 135 140	
Arg Gln Leu Gln Glu Gln Gln Arg Gln Lys Glu Leu Glu Arg Glu Arg	
145 150 155 160	
Met Glu Arg Glu Arg Leu Glu Arg Glu Arg Leu Glu Arg Glu Arg Leu	
165 170 175	



Glu Arg Glu Arg Leu Glu Gln Glu Gln Leu Glu Arg Gln Arg Gln Glu  
 180 185 190  
 Arg Glu His Val Glu Arg Leu Glu Arg Glu Arg Leu Glu Arg Leu Glu  
 195 200 205  
 Arg Glu Arg Gln Glu Arg Glu Arg Glu Arg Leu Glu Gln Leu Glu Arg  
 210 215 220  
 Glu Gln Val Glu Trp Glu Arg Glu Arg Arg Met Ser Asn Ala Ala Ala  
 225 230 235 240  
 Pro Ala Ser Ala Glu Thr Pro Leu Asn Pro Glu Leu Gly Asp Ser Ser  
 245 250 255  
 Ala Ser Glu Pro Gly Leu Gln Ala Ala Ser Gln Pro Ala Glu Ser Pro  
 260 265 270  
 Thr Pro Gln Gly Leu Val Leu Gly Pro Pro Ala Pro Pro Pro Pro Pro  
 275 280 285  
 Pro Leu Pro Ser Gly Pro Ala Tyr Ala Ser Ala Leu Pro Pro Pro Pro  
 290 295 300  
 Gly Pro Pro Pro Pro Pro Pro Leu Pro Ser Thr Gly Pro Pro Pro Pro  
 305 310 315 320  
 Pro Pro Pro Pro Pro Pro Leu Pro Asn Gln Ala Pro Pro Pro Pro Pro  
 325 330 335  
 Pro Pro Pro Ala Pro Pro Leu Pro Ala Ser Gly Ile Phe Ser Gly Ser  
 340 345 350  
 Thr Ser Glu Asp Asn Arg Pro Leu Thr Gly Leu Ala Ala Ala Ile Ala  
 355 360 365  
 Gly Ala Lys Leu Arg Lys Val Ser Arg Val Glu Asp Gly Ser Phe Pro  
 370 375 380  
 Gly Gly Gly Asn Thr Gly Ser Val Ser Leu Ala Ser Ser Lys Ala Asp  
 385 390 395 400  
 Ala Gly Arg Gly Asn Gly Pro Leu Pro Leu Gly Gly Ser Gly Leu Met  
 405 410 415  
 Glu Glu Met Ser Ala Leu Leu Ala Arg Arg Arg Arg Ile Ala Glu Lys  
 420 425 430  
 Gly Ser Thr Ile Glu Thr Glu Gln Lys Glu Asp Arg Asn Glu Asp Ala  
 435 440 445  
 Glu Pro Ile Thr Ala Lys Ala Pro Ser Thr Ser Thr Pro Glu Pro Thr  
 450 455 460  
 Arg Lys Pro Trp Glu Arg Thr Asn Thr Met Asn Gly Ser Lys Ser Pro  
 465 470 475 480  
 Val Ile Ser Arg Pro Lys Ser Thr Pro Ser Ser Gln Pro Ser Ala Asn  
 485 490 495  
 Gly Val Gln Thr Glu Gly Leu Asp Tyr Asp Arg Leu Lys Gln Asp Ile  
 500 505 510  
 Leu Asp Glu Met Arg Lys Glu Leu Ala Lys Leu Lys Glu Glu Leu Ile  
 515 520 525

Asp Ala Ile Arg Gln Glu Leu Ser Lys Ser Asn Thr Ala  
 530 535 540

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2898 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mus musculus*

## (vii) IMMEDIATE SOURCE:

- (B) CLONE: Neural Mena

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 140..2491

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TCGAGATTTA CCGTAACCCG CCCGCCGGAG CCGGACCCGC CTCTGCTCGC GCGTCCCCGC	60
GGCGTCCGCC TCCCCGCCTG AGAAGAGACC CTCGCTCGG CGGCTCCGC GCCGGGAAG	120
CCTCGGCGCC GCCGGCACCA TGAGTGAACA GAGTATCTGT CAGGCAAGAG CTGCTGTGAT	180
GGTCTATGAT GATGCCAATA AGAAGTGGGT GCCAGCTGGT GGCTCAACTG GGTTCAAGCAG	240
AGTACATATA TATCACCATA CAGGCAACAA CACATTGAGA GTTGTGGGCA GAAAGATTCA	300
AGACCATCAG GTTGTGATAA ACTGTGCCAT TCCTAAAGGG CTGAAGTACA ATCAAGCTAC	360
ACAGACTTTC CACCAATGGA GGGATGCTAG ACAGGTGTAT GGTCTCAACT TTGGCAGCAA	420
AGAGGATGCC AATGTCTTCG CAAGTGCCAT GATGCATGCC TTAGAAGTGT TAAATTGACA	480
GGAAGCAGGG CCAACATTGC CTAGACAAA TTCACAGCTA CCTGCTCAAG TTCAAATGG	540
CCCATCCCAA GAAGAGCTGG AAATCCAGAG AAGGCAACTG CAAGAACAGC AGCGACAGAA	600
GGAAGTGGAG AGGGAAAGAA TGGAGAGGGA AAGGTTGGAG AGAGAACGAC TAGAACGAGA	660
GAGGCTAGAG AGGGAGCGCC TGGAACAAGA GCAGCTGGAG CGGCAGCGGC AGGAAAGGGA	720
GCACGTGGAG CGGCTGGAGA GGGAGAGGCT GGAGCGCCTG GAGCGAGAGA GGCAGGAGCG	780
GGAGCGAGAG CGCCTGGAGC AGCTGGAGCG GGAGCAAGTG GAGTGGGAGC GAGAGCGCAG	840
AATGTCCAAT GCTGCTCCAT CTTGAGACAG CTCCCTGTCT AGTGCTCCAC TTCCTGAGTA	900
TTCCAGTTGC CAGCCGCCTT CGGCACCTCC TCCATCATAT GCTAAAGTCA TCTCAGCTCC	960
GGTGTGAGAC GCCACTCCTG ATTACGCTGT AGTGACTGCT TTGCCACCTA CTTCCACACC	1020
CCCTACACCA CCACTGAGAC ACGCAGCGAC ACGTTTTGCA ACATCTCTAG GTTCAGCCTT	1080
CCACCCTGTT CTTCCCCATT ACGCTACAGT TCCTCGTCCT CTCAACAAAA ACTCTCGACC	1140
TTCTTCTCCT GTGAACACAC CCTCTTCTCA GCCTCCAGCT GCGAAGTCCT GTGCCTGGCC	1200

TACTTCCAAT TTCTCGCCCC TCCCTCCATC TCCTCCAATA ATGATTAGCA GCCCCCTGG	1260
CAAAGCTACT GGNCCACGGC CTGTCCCTTCC CGTTTGTGTC TCCTCTCCTG TGCCCCAAAT	1320
GCCTCCGTCA CCAACAGCAC CCAATGGGTC GCTAGACTCT GTAACATACC CAGTGTCTCC	1380
ACCGCCTACC TCAGGGCCAG CAGCGCCACC TCCGCCGCCA CCGCCACCGC CGCCGCCACC	1440
ACCACCGCCG CTGCCACCGC CGCCGCTGCC TCCCCTCGCC TCACTCTCAC ACTGTGGATC	1500
ACAGGCTTCT CCTCCTCCAG GCACCCCTCT TGCCTCAACT CCCTCATCCA AGCCCAGTGT	1560
TCTCCCTTCT CCCTCTGCAG GTGCCCCCTGC CTCTGCGGAG ACCCCTCTAA ATCCTGAGCT	1620
GGGAGACTCC TCTGCTTCCG AGCCAGGCTT GCAGGCAGCC TCTCAGCCGG CCGAGTCGCC	1680
AACCCACAG GGCCTTGTCT TGGGACCACC TGCACCTCCG CCACCACCCC CTCTCCCATC	1740
AGGCCCTGCC TACGCCTCAG CACTTCCTCC TCCCCAGGA CCCCCTCCAC CACCTCCACT	1800
GCCATCCACT GGTCTCTCTC CTCCACCCCC TCCACCACCC CCTCTTCCTA ATCAAGCTCC	1860
TCCCCCTCCT CCCCCACCTC CTGCCCTCC CCTCCCCGCA TCTGGAATTT TCTCTGGATC	1920
CACGTCAGAA GACAATCGCC CTTTAACTGG ACTTGCAGCT GCAATTGCGG GAGCAAACT	1980
TAGGAAAGTG TCCCGGTGG AGGATGGCTC TTTCCCAGGT GGAGGGAATA CTGGGAGTGT	2040
GAGCTTGGCC TCATCCAAAG CAGACGCTGG GCGTGGGAAT GGACCTCTTC CTCTAGGGGG	2100
TAGTGGCTTA ATGGAAGAAA TGAGTGCCCT GCTGGCCAGG AGGAGAAGAA TTGCTGAGAA	2160
GGGATCAACA ATAGAAACAG AACAAAAGGA AGACAGAAAT GAAGATGCAG AGCCTATAAC	2220
TGCTAAGGCC CCATCAACAA GTACACCTGA ACCAACCAGA AAACCTTGGG AAAGAACAAA	2280
CACAATGAAC GGCAGTAAGT CACCTGTCAT CTCCAGACCC AAATCCACAC CTTCATCACA	2340
GCCAAGTGCC AATGGAGTCC AGACAGAAGG CCTTGACTAT GACAGGCTGA AGCAGGACAT	2400
TTTAGATGAG ATGAGAAAAG AGCTGGCAAA GCTGAAGGAG GAGCTTATTG ACGCAATCAG	2460
GCAGGAGCTG AGCAAGTCGA ACACTGCATA AAGAAGCAAA CTACGGAGGG GCAGGACTTG	2520
AATCTGGAGA AAACAAAAT TCCTACAAAC AACTCTTAAC CCCCAACTT TTAAGCTGTA	2580
AGAAGAAAAT GGATACACAG TCAGGAGGGA AGCCGTCAAC CTCTGAAAGC CTCAGACAGT	2640
GACTCTGGCG ATCAGCTGTC CCCTCAGTGT GCTGCTTTAT TCTGTCTGAC CTTTACCACA	2700
GGATGGAGAA TGATATTGGA GTTCCCTTAG CAGTACTAAA CCCGTCAGGC AAGATCACCG	2760
TGCATTGAAA TATTTTCATG TCTAGATGAG TCTGCACGTT TTCCATAATC CATTGCTAAA	2820
ATAAAGACGA GAAAGGGTAA ATCTCGAGGA ATTCATAATT TTTTCCTCCA GATCCTCTAG	2880
AGTCCTGTTT CCTGTGTG	2898

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 783 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (vii) IMMEDIATE SOURCE:

(B) CLONE: Neural Mena+ Deduced Amino Acid Sequence

## (ix) FEATURE:

(A) NAME/KEY: Region

(B) LOCATION: 239..482

(D) OTHER INFORMATION: /label= insertion

/note= "Inserted amino acids common to neural  
Mena+, neural Mena++, and neural Mena++"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```

Met Ser Glu Gln Ser Ile Cys Gln Ala Arg Ala Ala Val Met Val Tyr
 1           5           10           15
Asp Asp Ala Asn Lys Lys Trp Val Pro Ala Gly Gly Ser Thr Gly Phe
 20           25           30
Ser Arg Val His Ile Tyr His His Thr Gly Asn Asn Thr Phe Arg Val
 35           40           45
Val Gly Arg Lys Ile Gln Asp His Gln Val Val Ile Asn Cys Ala Ile
 50           55           60
Pro Lys Gly Leu Lys Tyr Asn Gln Ala Thr Gln Thr Phe His Gln Trp
 65           70           75           80
Arg Asp Ala Arg Gln Val Tyr Gly Leu Asn Phe Gly Ser Lys Glu Asp
 85           90           95
Ala Asn Val Phe Ala Ser Ala Met Met His Ala Leu Glu Val Leu Asn
100          105          110
Ser Gln Glu Ala Gly Pro Thr Leu Pro Arg Gln Asn Ser Gln Leu Pro
115          120          125
Ala Gln Val Gln Asn Gly Pro Ser Gln Glu Glu Leu Glu Ile Gln Arg
130          135          140
Arg Gln Leu Gln Glu Gln Gln Arg Gln Lys Glu Leu Glu Arg Glu Arg
145          150          155          160
Met Glu Arg Glu Arg Leu Glu Arg Glu Arg Leu Glu Arg Glu Arg Leu
165          170          175
Glu Arg Glu Arg Leu Glu Gln Glu Gln Leu Glu Arg Gln Arg Gln Glu
180          185          190
Arg Glu His Val Glu Arg Leu Glu Arg Glu Arg Leu Glu Arg Leu Glu
195          200          205
Arg Glu Arg Gln Glu Arg Glu Arg Glu Arg Leu Glu Gln Leu Glu Arg
210          215          220
Glu Gln Val Glu Trp Glu Arg Glu Arg Arg Met Ser Asn Ala Ala Pro
225          230          235          240
Ser Ser Asp Ser Ser Leu Ser Ser Ala Pro Leu Pro Glu Tyr Ser Ser
245          250          255
Cys Gln Pro Pro Ser Ala Pro Pro Pro Ser Tyr Ala Lys Val Ile Ser
260          265          270
Ala Pro Val Ser Asp Ala Thr Pro Asp Tyr Ala Val Val Thr Ala Leu
275          280          285

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Pro Pro Thr Ser Thr Pro Pro Thr Pro Pro Leu Arg His Ala Ala Thr  
 290 295 300  
 Arg Phe Ala Thr Ser Leu Gly Ser Ala Phe His Pro Val Leu Pro His  
 305 310 315 320  
 Tyr Ala Thr Val Pro Arg Pro Leu Asn Lys Asn Ser Arg Pro Ser Ser  
 325 330 335  
 Pro Val Asn Thr Pro Ser Ser Gln Pro Pro Ala Ala Lys Ser Cys Ala  
 340 345 350  
 Trp Pro Thr Ser Asn Phe Ser Pro Leu Pro Pro Ser Pro Pro Ile Met  
 355 360 365  
 Ile Ser Ser Pro Pro Gly Lys Ala Thr Gly Pro Arg Pro Val Leu Pro  
 370 375 380  
 Val Cys Val Ser Ser Pro Val Pro Gln Met Pro Pro Ser Pro Thr Ala  
 385 390 395 400  
 Pro Asn Gly Ser Leu Asp Ser Val Thr Tyr Pro Val Ser Pro Pro Pro  
 405 410 415  
 Thr Ser Gly Pro Ala Ala Pro Pro Pro Pro Pro Pro Pro Pro Pro  
 420 425 430  
 Pro Pro Pro Pro Pro Leu Pro Pro Pro Pro Leu Pro Pro Leu Ala Ser  
 435 440 445  
 Leu Ser His Cys Gly Ser Gln Ala Ser Pro Pro Pro Gly Thr Pro Leu  
 450 455 460  
 Ala Ser Thr Pro Ser Ser Lys Pro Ser Val Leu Pro Ser Pro Ser Ala  
 465 470 475 480  
 Gly Ala Pro Ala Ser Ala Glu Thr Pro Leu Asn Pro Glu Leu Gly Asp  
 485 490 495  
 Ser Ser Ala Ser Glu Pro Gly Leu Gln Ala Ala Ser Gln Pro Ala Glu  
 500 505 510  
 Ser Pro Thr Pro Gln Gly Leu Val Leu Gly Pro Pro Ala Pro Pro Pro  
 515 520 525  
 Pro Pro Pro Leu Pro Ser Gly Pro Ala Tyr Ala Ser Ala Leu Pro Pro  
 530 535 540  
 Pro Pro Gly Pro Pro Pro Pro Pro Pro Leu Pro Ser Thr Gly Pro Pro  
 545 550 555 560  
 Pro Pro Pro Pro Pro Pro Pro Pro Leu Pro Asn Gln Ala Pro Pro Pro  
 565 570 575  
 Pro Pro Pro Pro Pro Ala Pro Pro Leu Pro Ala Ser Gly Ile Phe Ser  
 580 585 590  
 Gly Ser Thr Ser Glu Asp Asn Arg Pro Leu Thr Gly Leu Ala Ala Ala  
 595 600 605  
 Ile Ala Gly Ala Lys Leu Arg Lys Val Ser Arg Val Glu Asp Gly Ser  
 610 615 620  
 Phe Pro Gly Gly Gly Asn Thr Gly Ser Val Ser Leu Ala Ser Ser Lys  
 625 630 635 640

Ala	Asp	Ala	Gly	Arg	Gly	Asn	Gly	Pro	Leu	Pro	Leu	Gly	Gly	Ser	Gly
				645					650						655
Leu	Met	Glu	Glu	Met	Ser	Ala	Leu	Leu	Ala	Arg	Arg	Arg	Arg	Ile	Ala
			660					665					670		
Glu	Lys	Gly	Ser	Thr	Ile	Glu	Thr	Glu	Gln	Lys	Glu	Asp	Arg	Asn	Glu
		675					680					685			
Asp	Ala	Glu	Pro	Ile	Thr	Ala	Lys	Ala	Pro	Ser	Thr	Ser	Thr	Pro	Glu
		690				695					700				
Pro	Thr	Arg	Lys	Pro	Trp	Glu	Arg	Thr	Asn	Thr	Met	Asn	Gly	Ser	Lys
705					710					715					720
Ser	Pro	Val	Ile	Ser	Arg	Pro	Lys	Ser	Thr	Pro	Ser	Ser	Gln	Pro	Ser
				725					730					735	
Ala	Asn	Gly	Val	Gln	Thr	Glu	Gly	Leu	Asp	Tyr	Asp	Arg	Leu	Lys	Gln
			740					745					750		
Asp	Ile	Leu	Asp	Glu	Met	Arg	Lys	Glu	Leu	Ala	Lys	Leu	Lys	Glu	Glu
		755					760					765			
Leu	Ile	Asp	Ala	Ile	Arg	Gln	Glu	Leu	Ser	Lys	Ser	Asn	Thr	Ala	
	770					775					780				

(2) INFORMATION FOR SEQ ID NO:5:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 787 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

- (B) CLONE: Neural Menatt

**(ix) FEATURE:**

- (A) NAME/KEY: Region  
(B) LOCATION: 117..119  
(D) OTHER INFORMATION: /label= Insertion  
/note= "Inserted amino acids in neural Mena++"

(ix) **FEATURE:**

- (A) NAME/KEY: Region  
(B) LOCATION: 239..482  
(D) OTHER INFORMATION: /label= insertion  
/note= "Inserted amino acids common to neural  
Menat+, neural Menat++ and Neural Menat+++"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Ser	Glu	Gln	Ser	Ile	Cys	Gln	Ala	Arg	Ala	Ala	Val	Met	Val	Tyr
1				5					10					15	
Asp	Asp	Ala	Asn	Lys	Lys	Trp	Val	Pro	Ala	Gly	Gly	Ser	Thr	Gly	Phe
			20					25					30		
Ser	Arg	Val	His	Ile	Tyr	His	His	Thr	Gly	Asn	Asn	Thr	Phe	Arg	Val
		35					40					45			
Val	Gly	Arg	Lys	Ile	Gln	Asp	His	Gln	Val	Val	Ile	Asn	Cys	Ala	Ile
	50					55					60				

Pro Lys Gly Leu Lys Tyr Asn Gln Ala Thr Gln Thr Phe His Gln Trp  
 65 70 75 80  
 Arg Asp Ala Arg Gln Val Tyr Gly Leu Asn Phe Gly Ser Lys Glu Asp  
 85 90 95  
 Ala Asn Val Phe Ala Ser Ala Met Met His Ala Leu Glu Val Leu Asn  
 100 105 110  
 Ser Gln Glu Ala Val Phe Tyr Leu Gly Pro Thr Leu Pro Arg Gln Asn  
 115 120 125  
 Ser Gln Leu Pro Ala Gln Val Gln Asn Gly Pro Ser Gln Glu Glu Leu  
 130 135 140  
 Glu Ile Gln Arg Arg Gln Leu Gln Glu Gln Gln Arg Gln Lys Glu Leu  
 145 150 155 160  
 Glu Arg Glu Arg Met Glu Arg Glu Arg Leu Glu Arg Glu Arg Leu Glu  
 165 170 175  
 Arg Glu Arg Leu Glu Arg Glu Arg Leu Glu Gln Glu Gln Leu Glu Arg  
 180 185 190  
 Gln Arg Gln Glu Arg Glu His Val Glu Arg Leu Glu Arg Glu Arg Leu  
 195 200 205  
 Glu Arg Leu Glu Arg Glu Arg Gln Glu Arg Glu Arg Glu Arg Leu Glu  
 210 215 220  
 Gln Leu Glu Arg Glu Gln Val Glu Trp Glu Arg Glu Arg Arg Met Ser  
 225 230 235 240  
 Asn Ala Ala Pro Ser Ser Asp Ser Ser Leu Ser Ser Ala Pro Leu Pro  
 245 250 255  
 Glu Tyr Ser Ser Cys Gln Pro Pro Ser Ala Pro Pro Pro Ser Tyr Ala  
 260 265 270  
 Lys Val Ile Ser Ala Pro Val Ser Asp Ala Thr Pro Asp Tyr Ala Val  
 275 280 285  
 Val Thr Ala Leu Pro Pro Thr Ser Thr Pro Pro Thr Pro Pro Leu Arg  
 290 295 300  
 His Ala Ala Thr Arg Phe Ala Thr Ser Leu Gly Ser Ala Phe His Pro  
 305 310 315 320  
 Val Leu Pro His Tyr Ala Thr Val Pro Arg Pro Leu Asn Lys Asn Ser  
 325 330 335  
 Arg Pro Ser Ser Pro Val Asn Thr Pro Ser Ser Gln Pro Pro Ala Ala  
 340 345 350  
 Lys Ser Cys Ala Trp Pro Thr Ser Asn Phe Ser Pro Leu Pro Pro Ser  
 355 360 365  
 Pro Pro Ile Met Ile Ser Ser Pro Pro Gly Lys Ala Thr Gly Pro Arg  
 370 375 380  
 Pro Val Leu Pro Val Cys Val Ser Ser Pro Val Pro Gln Met Pro Pro  
 385 390 395 400  
 Ser Pro Thr Ala Pro Asn Gly Ser Leu Asp Ser Val Thr Tyr Pro Val  
 405 410 415

Ser Pro Pro Pr Thr Ser Gly Pro Ala Ala Pro Pro Pro Pro Pro Pro  
 420 425 430  
 Pro Pro Pro Pro Pro Pro Pro Pro Pro Leu Pro Pro Pro Pro Leu Pro  
 435 440 445  
 Pro Leu Ala Ser Leu Ser His Cys Gly Ser Gln Ala Ser Pro Pro Pro  
 450 455 460  
 Gly Thr Pro Leu Ala Ser Thr Pro Ser Ser Lys Pro Ser Val Leu Pro  
 465 470 475 480  
 Ser Pro Ser Ala Gly Ala Pro Ala Ser Ala Glu Thr Pro Leu Asn Pro  
 485 490 495  
 Glu Leu Gly Asp Ser Ser Ala Ser Glu Pro Gly Leu Gln Ala Ala Ser  
 500 505 510  
 Gln Pro Ala Glu Ser Pro Thr Pro Gln Gly Leu Val Leu Gly Pro Pro  
 515 520 525  
 Ala Pro Pro Pro Pro Pro Pro Leu Pro Ser Gly Pro Ala Tyr Ala Ser  
 530 535 540  
 Ala Leu Pro Pro Pro Pro Gly Pro Pro Pro Pro Pro Pro Leu Pro Ser  
 545 550 555 560  
 Thr Gly Pro Pro Pro Pro Pro Pro Pro Pro Pro Pro Leu Pro Asn Gln  
 565 570 575  
 Ala Pro Pro Pro Pro Pro Pro Pro Ala Pro Pro Leu Pro Ala Ser  
 580 585 590  
 Gly Ile Phe Ser Gly Ser Thr Ser Glu Asp Asn Arg Pro Leu Thr Gly  
 595 600 605  
 Leu Ala Ala Ala Ile Ala Gly Ala Lys Leu Arg Lys Val Ser Arg Val  
 610 615 620  
 Glu Asp Gly Ser Phe Pro Gly Gly Gly Asn Thr Gly Ser Val Ser Leu  
 625 630 635 640  
 Ala Ser Ser Lys Ala Asp Ala Gly Arg Gly Asn Gly Pro Leu Pro Leu  
 645 650 655  
 Gly Gly Ser Gly Leu Met Glu Glu Met Ser Ala Leu Leu Ala Arg Arg  
 660 665 670  
 Arg Arg Ile Ala Glu Lys Gly Ser Thr Ile Glu Thr Glu Gln Lys Glu  
 675 680 685  
 Asp Arg Asn Glu Asp Ala Glu Pro Ile Thr Ala Lys Ala Pro Ser Thr  
 690 695 700  
 Ser Thr Pro Glu Pro Thr Arg Lys Pro Trp Glu Arg Thr Asn Thr Met  
 705 710 715 720  
 Asn Gly Ser Lys Ser Pro Val Ile Ser Arg Pro Lys Ser Thr Pro Ser  
 725 730 735  
 Ser Gln Pro Ser Ala Asn Gly Val Gln Thr Glu Gly Leu Asp Tyr Asp  
 740 745 750  
 Arg Leu Lys Gln Asp Ile Leu Asp Glu Met Arg Lys Glu Leu Ala Lys  
 755 760 765



Leu Lys Glu Glu Leu Ile Asp Ala Ile Arg Gln Glu Leu Ser Lys Ser  
 770 775 780

Asn Thr Ala  
 785

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 802 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

- (B) CLONE: Neural Mena+++

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 117..135
- (D) OTHER INFORMATION: /label= Insertion  
 /note= "Inserted amino acids in neural Mena  
 Isoform 2"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 239..482
- (D) OTHER INFORMATION: /label= insertion  
 /note= "Inserted amino acids common to neural  
 Mena+, neural Mena++ and neural Mena+++"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Ser	Glu	Gln	Ser	Ile	Cys	Gln	Ala	Arg	Ala	Ala	Val	Met	Val	Tyr
1				5					10					15	
Asp	Asp	Ala	Asn	Lys	Lys	Trp	Val	Pro	Ala	Gly	Gly	Ser	Thr	Gly	Phe
			20					25						30	
Ser	Arg	Val	His	Ile	Tyr	His	His	Thr	Gly	Asn	Asn	Thr	Phe	Arg	Val
			35				40					45			
Val	Gly	Arg	Lys	Ile	Gln	Asp	His	Gln	Val	Val	Ile	Asn	Cys	Ala	Ile
			50			55						60			
Pro	Lys	Gly	Leu	Lys	Tyr	Asn	Gln	Ala	Thr	Gln	Thr	Phe	His	Gln	Trp
65					70					75					80
Arg	Asp	Ala	Arg	Gln	Val	Tyr	Gly	Leu	Asn	Phe	Gly	Ser	Lys	Glu	Asp
				85					90					95	
Ala	Asn	Val	Phe	Ala	Ser	Ala	Met	Met	His	Ala	Leu	Glu	Val	Leu	Asn
				100				105						110	
Ser	Gln	Glu	Ala	Ala	Gln	Ser	Lys	Val	Thr	Ala	Thr	Gln	Asp	Ser	Thr
				115				120					125		
Asn	Leu	Arg	Cys	Ile	Phe	Cys	Gly	Pro	Thr	Leu	Pro	Arg	Gln	Asn	Ser
				130			135					140			
Gln	Leu	Pro	Ala	Gln	Val	Gln	Asn	Gly	Pro	Ser	Gln	Glu	Glu	Leu	Glu
145					150					155					160

Ile Gln Arg Arg Gln Leu Gln Glu Gln Gln Arg Gln Lys Glu Leu Glu  
 165 170 175  
 Arg Glu Arg Met Glu Arg Glu Arg Leu Glu Arg Glu Arg Leu Glu Arg  
 180 185 190  
 Glu Arg Leu Glu Arg Glu Arg Leu Glu Gln Glu Gln Leu Glu Arg Gln  
 195 200 205  
 Arg Gln Glu Arg Glu His Val Glu Arg Leu Glu Arg Glu Arg Leu Glu  
 210 215 220  
 Arg Leu Glu Arg Glu Arg Gln Glu Arg Glu Arg Glu Arg Leu Glu Gln  
 225 230 235 240  
 Leu Glu Arg Glu Gln Val Glu Trp Glu Arg Glu Arg Arg Met Ser Asn  
 245 250 255  
 Ala Ala Pro Ser Ser Asp Ser Ser Leu Ser Ser Ala Pro Leu Pro Glu  
 260 265 270  
 Tyr Ser Ser Cys Gln Pro Pro Ser Ala Pro Pro Pro Ser Tyr Ala Lys  
 275 280 285  
 Val Ile Ser Ala Pro Val Ser Asp Ala Thr Pro Asp Tyr Ala Val Val  
 290 295 300  
 Thr Ala Leu Pro Pro Thr Ser Thr Pro Pro Thr Pro Pro Leu Arg His  
 305 310 315 320  
 Ala Ala Thr Arg Phe Ala Thr Ser Leu Gly Ser Ala Phe His Pro Val  
 325 330 335  
 Leu Pro His Tyr Ala Thr Val Pro Arg Pro Leu Asn Lys Asn Ser Arg  
 340 345 350  
 Pro Ser Ser Pro Val Asn Thr Pro Ser Ser Gln Pro Pro Ala Ala Lys  
 355 360 365  
 Ser Cys Ala Trp Pro Thr Ser Asn Phe Ser Pro Leu Pro Pro Ser Pro  
 370 375 380  
 Pro Ile Met Ile Ser Ser Pro Pro Gly Lys Ala Thr Gly Pro Arg Pro  
 385 390 395 400  
 Val Leu Pro Val Cys Val Ser Ser Pro Val Pro Gln Met Pro Pro Ser  
 405 410 415  
 Pro Thr Ala Pro Asn Gly Ser Leu Asp Ser Val Thr Tyr Pro Val Ser  
 420 425 430  
 Pro Pro Pro Thr Ser Gly Pro Ala Ala Pro Pro Pro Pro Pro Pro Pro  
 435 440 445  
 Pro Pro Pro Pro Pro Pro Pro Leu Pro Pro Pro Pro Leu Pro Pro  
 450 455 460  
 Leu Ala Ser Leu Ser His Cys Gly Ser Gln Ala Ser Pro Pro Pro Gly  
 465 470 475 480  
 Thr Pro Leu Ala Ser Thr Pro Ser Ser Lys Pro Ser Val Leu Pro Ser  
 485 490 495  
 Pro Ser Ala Gly Ala Pro Ala Ser Ala Glu Thr Pro Leu Asn Pro Glu  
 500 505 510

Leu Gly Asp Ser Ser Ala Ser Glu Pro Gly Leu Gln Ala Ala Ser Gln  
 515 520 525  
 Pro Ala Glu Ser Pro Thr Pro Gln Gly Leu Val Leu Gly Pro Pro Ala  
 530 535 540  
 Pro Pro Pro Pro Pro Pro Leu Pro Ser Gly Pro Ala Tyr Ala Ser Ala  
 545 550 555 560  
 Leu Pro Pro Pro Pro Gly Pro Pro Pro Pro Pro Pro Leu Pro Ser Thr  
 565 570 575  
 Gly Pro Pro Pro Pro Pro Pro Pro Pro Pro Pro Leu Pro Asn Gln Ala  
 580 585 590  
 Pro Pro Pro Pro Pro Pro Pro Pro Ala Pro Pro Leu Pro Ala Ser Gly  
 595 600 605  
 Ile Phe Ser Gly Ser Thr Ser Glu Asp Asn Arg Pro Leu Thr Gly Leu  
 610 615 620  
 Ala Ala Ala Ile Ala Gly Ala Lys Leu Arg Lys Val Ser Arg Val Glu  
 625 630 635 640  
 Asp Gly Ser Phe Pro Gly Gly Gly Asn Thr Gly Ser Val Ser Leu Ala  
 645 650 655  
 Ser Ser Lys Ala Asp Ala Gly Arg Gly Asn Gly Pro Leu Pro Leu Gly  
 660 665 670  
 Gly Ser Gly Leu Met Glu Glu Met Ser Ala Leu Leu Ala Arg Arg Arg  
 675 680 685  
 Arg Ile Ala Glu Lys Gly Ser Thr Ile Glu Thr Glu Gln Lys Glu Asp  
 690 695 700  
 Arg Asn Glu Asp Ala Glu Pro Ile Thr Ala Lys Ala Pro Ser Thr Ser  
 705 710 715 720  
 Thr Pro Glu Pro Thr Arg Lys Pro Trp Glu Arg Thr Asn Thr Met Asn  
 725 730 735  
 Gly Ser Lys Ser Pro Val Ile Ser Arg Pro Lys Ser Thr Pro Ser Ser  
 740 745 750  
 Gln Pro Ser Ala Asn Gly Val Gln Thr Glu Gly Leu Asp Tyr Asp Arg  
 755 760 765  
 Leu Lys Gln Asp Ile Leu Asp Glu Met Arg Lys Glu Leu Ala Lys Leu  
 770 775 780  
 Lys Glu Glu Leu Ile Asp Ala Ile Arg Gln Glu Leu Ser Lys Ser Asn  
 785 790 795 800  
 Thr Ala

## (2) INFORMATION FOR SEQ ID NO:7:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1956 bas pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mus musculus*

## (vii) IMMEDIATE SOURCE:

(B) CLONE: Ev1

## (ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 418..1599

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AGCTGGCGAA AGGGGATGTG CTGCAAGGCG ATTAAGTTGG TAACGCCAGG TTTTCCCAGT	60
CANGACGTTG TAAACGACG GCCAGTGAAT TGTAATACGA CTCACTATAG GGCGAATTGG	120
TACCGGGCCC CCCTTCGAGG TCGACGGTAT CGATAAGCTT GATATGCGCC GGCCCGGGCA	180
CGCGCGCCCG CCAAGATGGC AGGGGCGGGG GCCCAGNTGT CAGTCGCCAC CGCCGCCGCC	240
GCGGCGGGCG CGTTGCTTCG CAGCTAGCGG CCCGGACGCC CGCCGGAGAA GATGAGCCCC	300
CGCCGCCGCN TGCAGCCCAG CCAGACGCGG AGCCGCCGCG CCCGGGGTCG GCTGCCCCGC	360
TAGCGTCCCG TCGCGCCGCG CTTTCATCCC CGGCCCCGTG CCCGCCCGGC AGCCACGATG	420
AGTGAACAGA GATCTGCCA AGCGCGGGCC TCCGTGATGG TCTACGATGA CACCAGTAAG	480
AAGTGGGTAC CGATCAAGCC TGGCCAGCAG GGATTCAGCC GGATCAACAT CTACCACAAC	540
ACTGCCAGCA GCACCTTCAG AGTGGTCGGG GTCAAGCTAC AGGACCAGCA GGTGTGTATC	600
AATTATTCAA TTGTTAAAGG GCTGAAGTAC AATCAGGCAA CACCCACCTT CCATCAGTGG	660
CGAGATGCCC GTCAGGTCTA TGGCTTAAAC TTTGCAAGTA AGGAAGAAGC AACCACATTC	720
TCCAATGCCA TGCTCTTTGC CCTGAACATC ATGAATTCCC AAGAAGGAGG CCCCTCCACA	780
CAGCGTCAGG TGCAGAATGG CCCCTCTCCT GAGGAGATGG ACATCCAGAG AAGACAAGTA	840
ATGGAGCAGC AGCACCGCCA GGAGTCTCTG GAGAGGAGAA TCTCGGCCAC AGGGCCCATT	900
CTCCCCCTG GGCATCCCTC ATCGGCAGCC AGCACCCTC TCTCCTGTAG TGGACCTCCA	960
CCCCCGCCTC CACCCCCAGT TCCACCTCCA CCCACAGGGT CTACTCCCCC ACCCCCACCC	1020
CCACTGCCAG CTGGAGGAGC CCAGGGGACC AACCATGATG AGAGCTCTGC ATCAGGACTG	1080
GCTGCTGCTC TGGCGGGAGC CAAGCTAAGG AGGGTGCAGC GGCCAGAAGA TGCATCTGGA	1140
GGTCCAGTC CTAGTGGGAC TTCAAAGTCC GATGCCAACC GGGCAAGCAG TGGGGGAGGT	1200
GGAGGAGGCC TCATGGAAGA AATGAACAAG CTGCTGGCTA AGAGGAGAAA GGCAGCCTCC	1260
CAGACAGACA AGCCCGCTGA CAGAAAGGAA GATGAGAGCC AAACGGAAGA CCCTAGCACC	1320
TCCCCATCCC CAGGTACCCG AGCCACCAGC CAGCCACCTA ATTCCTCAGA GGCTGGCAGA	1380
AAACCCTGGG AACGGAGCAA CTCGGTGGAG AAACCTGTGT CCTCGTTGCT GTCCAGGGTG	1440
AAGCCTGCTG GGAGTGTGAA TGACGTGGGC CTGGATGCCT TAGATTTGGA CCGGATGAAA	1500
CAGGAGATCC TGGAGGAGGT GGTTCGGGAG CTGCACAAGG TGAAGGAGGA GATCATTGAT	1560
GCCATCAGGC AGGAGCTAAG TGGGATCAGC ACCACGTAAG ATGGCACCAG TCCTGGAGGA	1620

TTGCGAGGAG CCGTGCTGGC CCCAGCGAGC ATCGAGCCTG CAGAAGCTGG GATGTACTTA 1680  
 AGTCTCAACC TGTGATACAA TCTTAAAATG AGGAAACAAA CTTCAACTCC TGGATTTTTT 1740  
 AGTGTATCTG ACACAGAACA CCGGGTCTAT TCTTTTTTTG TATTTTATAT TTGCTTATTT 1800  
 AAGTGTACGT TCCTTTGGTT TATAGAGAAC ACCCCCCAAT CACCTGCTTT ATTAGATGGC 1860  
 TTCCAAGTTT TCTCCTAGGT GACACTGTTG GTGCCTCAGC TGACAGGGAG CAGCTGGGTG 1920  
 CAGTGTGGCC TTTCCATGCC ACAGAGCTGT CAGAAT 1956

## (2) INFORMATION FOR SEQ ID NO:8:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (vii) IMMEDIATE SOURCE:

- (B) CLONE: Evl Deduced Amino Acid Sequence

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Ser Glu Gln Ser Ile Cys Gln Ala Arg Ala Ser Val Met Val Tyr  
 1 5 10 15  
 Asp Asp Thr Ser Lys Lys Trp Val Pro Ile Lys Pro Gly Gln Gln Gly  
 20 25 30  
 Phe Ser Arg Ile Asn Ile Tyr His Asn Thr Ala Ser Ser Thr Phe Arg  
 35 40 45  
 Val Val Gly Val Lys Leu Gln Asp Gln Gln Val Val Ile Asn Tyr Ser  
 50 55 60  
 Ile Val Lys Gly Leu Lys Tyr Asn Gln Ala Thr Pro Thr Phe His Gln  
 65 70 75 80  
 Trp Arg Asp Ala Arg Gln Val Tyr Gly Leu Asn Phe Ala Ser Lys Glu  
 85 90 95  
 Glu Ala Thr Thr Phe Ser Asn Ala Met Leu Phe Ala Leu Asn Ile Met  
 100 105 110  
 Asn Ser Gln Glu Gly Gly Pro Ser Thr Gln Arg Gln Val Gln Asn Gly  
 115 120 125  
 Pro Ser Pro Glu Glu Met Asp Ile Gln Arg Arg Gln Val Met Glu Gln  
 130 135 140  
 Gln His Arg Gln Glu Ser Leu Glu Arg Arg Ile Ser Ala Thr Gly Pro  
 145 150 155 160  
 Ile Leu Pro Pro Gly His Pro Ser Ser Ala Ala Ser Thr Thr Leu Ser  
 165 170 175  
 Cys Ser Gly Pro Pro Pro Pro Pro Pro Pro Val Pro Pro Pro Pro  
 180 185 190  
 Thr Gly Ser Thr Pro Pro Pro Pro Pro Pro Leu Pro Ala Gly Gly Ala  
 195 200 205

Gln Gly Thr Asn His Asp Glu Ser Ser Ala Ser Gly Leu Ala Ala Ala  
 210 215 220  
 Leu Ala Gly Ala Lys Leu Arg Arg Val Gln Arg Pro Glu Asp Ala Ser  
 225 230 235 240  
 Gly Gly Ser Ser Pro Ser Gly Thr Ser Lys Ser Asp Ala Asn Arg Ala  
 245 250 255  
 Ser Ser Gly Gly Gly Gly Gly Gly Leu Met Glu Glu Met Asn Lys Leu  
 260 265 270  
 Leu Ala Lys Arg Arg Lys Ala Ala Ser Gln Thr Asp Lys Pro Ala Asp  
 275 280 285  
 Arg Lys Glu Asp Glu Ser Gln Thr Glu Asp Pro Ser Thr Ser Pro Ser  
 290 295 300  
 Pro Gly Thr Arg Ala Thr Ser Gln Pro Pro Asn Ser Ser Glu Ala Gly  
 305 310 315 320  
 Arg Lys Pro Trp Glu Arg Ser Asn Ser Val Glu Lys Pro Val Ser Ser  
 325 330 335  
 Leu Leu Ser Arg Val Lys Pro Ala Gly Ser Val Asn Asp Val Gly Leu  
 340 345 350  
 Asp Ala Leu Asp Leu Asp Arg Met Lys Gln Glu Ile Leu Glu Glu Val  
 355 360 365  
 Val Arg Glu Leu His Lys Val Lys Glu Glu Ile Ile Asp Ala Ile Arg  
 370 375 380  
 Gln Glu Leu Ser Gly Ile Ser Thr Thr  
 385 390

## (2) INFORMATION FOR SEQ ID NO:9:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 740 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Ser Glu Gln Ser Ile Cys Xaa Ala Arg Ala Xaa Val Met Val Tyr  
 1 5 10 15  
 Asp Asp Xaa Xaa Lys Lys Trp Val Pro Xaa Xaa Xaa Gly Xaa Xaa Gly  
 20 25 30  
 Phe Ser Arg Val Xaa Ile Tyr His Xaa Xaa Xaa Xaa Asn Thr Phe Arg  
 35 40 45  
 Val Val Gly Arg Lys Leu Gln Xaa Asp Xaa Gln Val Val Ile Asn Cys  
 50 55 60  
 Xaa Ile Xaa Lys Gly Leu Lys Tyr Asn Gln Ala Thr Pro Thr Phe His  
 65 70 75 80  
 Gln Trp Arg Asp Ala Arg Gln Val Tyr Gly Leu Asn Phe Xaa Ser Lys  
 85 90 95  
 Glu Asp Ala Xaa Xaa Phe Ala Xaa Ala Met Xaa Xaa Ala Leu Glu Xaa  
 100 105 110

Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Pro Xaa Xaa Xaa  
 115 120 125  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Val Xaa Asn Gly Pro Ser  
 130 135 140  
 Xaa Glu Glu Xaa Xaa Xaa Gln Xaa Arg Gln Xaa Xaa Xaa Xaa Xaa Xaa  
 145 150 155 160  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 165 170 175  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 180 185 190  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 195 200 205  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 210 215 220  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Glu  
 225 230 235 240  
 Arg Arg Xaa Ser Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 245 250 255  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 260 265 270  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 275 280 285  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 290 295 300  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 305 310 315 320  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 325 330 335  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 340 345 350  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 355 360 365  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 370 375 380  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 385 390 395 400  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Pro Pro Ala  
 405 410 415  
 Pro Xaa Xaa Xaa Pro Xaa Xaa Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 420 425 430  
 Xaa Pro Pro Pro Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Pro Pro Pro  
 435 440 445  
 Pro Pro Xaa Xaa Xaa Xaa Xaa Gly Pro Pro Pro Xaa Pro Xaa Xaa Pro  
 450 455 460

Pro Xaa Xaa Xaa Pro Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Xaa Pro Pro  
 465 470 475 480  
 Pro Ala Pro Pro Leu Pro Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 485 490 495  
 Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 500 505 510  
 Xaa Gly Leu Ala Ala Ala Xaa Ala Gly Ala Lys Leu Arg Lys Val Xaa  
 515 520 525  
 Xaa Xaa Glu Xaa Ala Ser Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 530 535 540  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 545 550 555 560  
 Xaa Xaa Gly Gly Xaa Gly Leu Met Glu Glu Met Xaa Xaa Xaa Leu Ala  
 565 570 575  
 Arg Arg Arg Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 580 585 590  
 Lys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Pro Xaa Xaa Xaa Xaa Xaa Xaa  
 595 600 605  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Glu Xaa Xaa Arg  
 610 615 620  
 Xaa Pro Trp Glu Xaa Xaa Asn Thr Xaa Xaa Xaa Xaa Xaa Ser Xaa Xaa  
 625 630 635 640  
 Xaa Ser Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 645 650 655  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 660 665 670  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 675 680 685  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asp Leu  
 690 695 700  
 Asp Arg Xaa Lys Gln Glu Ile Leu Xaa Glu Xaa Xaa Xaa Glu Leu Xaa  
 705 710 715 720  
 Lys Val Lys Glu Glu Ile Ile Asp Ala Ile Xaa Gln Glu Leu Xaa Xaa  
 725 730 735  
 Xaa Xaa Xaa Xaa  
 740

## (2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 5 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Leu Glu Arg Glu Arg  
1 5

## (2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Leu Lys Glu Glu Leu Ile Asp Ala Ile Arg Gln Glu Leu Ser Lys Ser  
1 5 10 15

Asn Thr Ala

## (2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Ser Glu Pro Ser Ser Phe Glu Phe Pro Pro Pro Pro Thr Asp Glu Glu  
1 5 10 15

Leu Arg Leu Ala  
20

## (2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 6 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Gly Pro Pro Pro Pro Pro  
1 5

## (2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:  
(B) CLONE: MF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AATCGCACAC TCTGTCCATA TTCC

24

## (2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:  
(B) CLONE: MR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TGCCCCACAAC TCTGAATGTG TTG

23

## (2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:  
(B) CLONE: BPAF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TCCCAGTCAC GACGTTGTAA AAC

23

## (2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 5 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Phe	Pro	Pro	Pro	Pro
1				5

**CLAIMS**

**We claim:**

- 1. A screening method for detecting the presence in a test sample of a modulator of activity or expression of a Mena protein or peptide, comprising the steps of:**
  - providing a control sample including suitable amounts of Mena protein or peptide and a Mena binding partner under conditions that permit formation of complexes between the binding partner and the Mena protein or peptide;**
  - providing a test sample including a test substance and suitable amounts of Mena protein or peptide and a selected Mena-binding partner under conditions that permit formation of complexes between the binding partner and the Mena protein or peptide in the absence of the test substance;**
  - detecting complexes of Mena and Mena-binding partner in the test sample and in a control sample to determine whether the test substance is a modulator of activity or expression of the Mena protein or peptide.**

## INTERNATIONAL SEARCH REPORT

International application No.  
PCT/US97/11669

## A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) : G01N 33/53

US CL : 435/7.2

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/7.2; 530/350

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

APS, DIALOG (medline, dissertation abstracts, biosis, embase, derwent, life sciences, conference papers, cancerlit, CAS)

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X,P	GERTLER, F.B., "MENA, A RELATIVE OF VASP AND DROSOPHILA ENABLED, IS IMPLICATED IN THE CONTROL OF MICROFILAMNET DYNAMICS", CELL. 18 OCTOBER 1996. VOL 87. NO. 2. PAGES 227-239, SEE ENTIRE DOCUMENT.	1
A	ODDE, D.J., "KINETICS OF MICROTUBULE CATASTROPHE ASSESSED BY PROBABILISTIC ANALYSIS", BIOPHYS J, SEPTEMBER 1995, VOL 69. NO. 3. PAGES 796-802, SEE ENTIRE REFERENCE.	1
A	BLACK, M. M., "MICROTUBULE TRANSPORT AND ASSEMBLY COOPERATE TO GENERATE THE MICROTUBULE ARRAY OF GROWING AXONS", PROG BRAIN RES. 1994, VOL. 102, PAGES 61-77, SEE ENTIRE REFERENCE.	1



Further documents are listed in the continuation of Box C.



See patent family annex.

* Special categories of cited documents:	*T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
*A* document defining the general state of the art which is not considered to be of particular relevance	*X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
*E* earlier document published on or after the international filing date	*Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
*L* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	*A* document member of the same patent family
*O* document referring to an oral disclosure, use, exhibition or other means	
*P* document published prior to the international filing date but later than the priority date claimed	

Date of the actual completion of the international search

05 SEPTEMBER 1997

Date of mailing of the international search report

16 OCT 1997

Name and mailing address of the ISA/US  
Commissioner of Patents and Trademarks  
Box PCT  
Washington, D.C. 20231

Facsimile No. (703) 305-3230

Authorized officer

SUSAN A. LORING

Telephone No. (703) 308-00196

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: *Mus musculus*

(vii) IMMEDIATE SOURCE:  
(B) CLONE: Evl

(ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION: 418..1599

(xi) SEQUENCE DESCRIPTION: SEQ ID NO. 7:

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AGCTGGCGAA AGGGGATGTG CTGCAAGGCG ATTAAGTTGG TAACGCCAGG TTTTCCCAGT   60
CANGACGTTG TAAAACGACG GCCAGTGAAT TGTAATACGA CTCACTATAG GGCGAATTGG  120
TACCGGGCCC CCCTTCGAGG TCGACGGTAT CGATAAGCTT GATATGCGCC GGCCCGGGCA  180
CGCGCGCCCC CCAAGATGGC AGGGGCCGGG GCCCAGNTGT CAGTCGCCAC CGCCGCCGCC  240
GCGGCGGGCC CGTTGCTTCG CAGCTAGCGG CCCGGACGCC CGCCGGAGAA GATGAGCCCC  300
CGCCGCCGCN TGCAGCCCAG CCAGACGCGG AGCCGCCGCG CCCGGGGTCG GCTGCCCCGC  360
TAGCGTCCCG TCGCGCCGCG CTTTCATCCC CGGCCCCGTG CCCGCCCGGC AGCCACGATG  420
AGTGAACAGA GTATCTGCCA AGCGCGGGCC TCCGTGATGG TCTACGATGA CACCAGTAAG  480
AAGTGGGTAC CGATCAAGCC TGGCCAGCAG GGATTCAGCC GGATCAACAT CTACCACAAC  540
ACTGCCAGCA GCACCTTCAG AGTGGTCGGG GTCAAGCTAC AGGACCAGCA GGTTGTGATC  600
AATTATTCAA TTGTTAAAGG GCTGAAGTAC AATCAGGCAA CACCCACCTT CCATCAGTGG  660
CGAGATGCCC GTCAGGTCTA TGGCTTAAAC TTTGCAAGTA AGGAAGAAGC AACCACATTC  720
TCCAATGCCA TGCTCTTTGC CCTGAACATC ATGAATTCCC AAGAAGGAGG CCCCTCCACA  780
CAGCGTCAGG TGCAGAATGG CCCCTCTCCT GAGGAGATGG ACATCCAGAG AAGACAAGTA  840
ATGGAGCAGC AGCACCGCCA GGAGTCTCTG GAGAGGAGAA TCTCGGCCAC AGGGCCCAT  900
CTCCCCCTG GGCATCCCTC ATCGGCAGCC AGCACCCTC TCTCCTGTAG TGGACCTCCA  960
CCCCCGCTC CACCCCCAGT TCCACCTCCA CCCACAGGGT CTACTCCCCC ACCCCCACCC 1020
CCACTGCCAG CTGGAGGAGC CCAGGGGACC AACCATGATG AGAGCTCTGC ATCAGGACTG 1080
GCTGCTGCTC TGGCGGGAGC CAAGCTAAGG AGGGTGCAGC GGCCAGAAGA TGCATCTGGA 1140
GGCTCCAGTC CTAGTGGGAC TTCAAAGTCC GATGCCAACC GGGCAAGCAG TGGGGGAGGT 1200
GGAGGAGGCC TCATGGAAGA AATGAACAAG CTGCTGGCTA AGAGGAGAAA GGCAGCCTCC 1260
CAGACAGACA AGCCCGCTGA CAGAAAGGAA GATGAGAGCC AAACGGAAGA CCCTAGCACC 1320
TCCCCATCCC CAGGTACCCG AGCCACCAGC CAGCCACCTA ATTCCTCAGA GGCTGGCAGA 1380
AAACCCTGGG AACGGAGCAA CTCGGTGGAG AAACCTGTGT CCTCGTTGCT GTCCAGGGTG 1440
AAGCCTGCTG GGAGTGTGAA TGACGTGGGC CTGGATGCCT TAGATTGGA CCGGATGAAA 1500
CAGGAGATCC TGGAGGAGGT GGTTCGGGAG CTGCACAAGG TGAAGGAGGA GATCATTGAT 1560
GCCATCAGGC AGGAGCTAAG TGGGATCAGC ACCACGTAAG ATGGCACCAG TCCTGGAGGA 1620

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TTGCGAGGAG CCGTGCTGGC CCCAGCGAGC ATCGAGCCTG CAGAAGCTGG CATGTACTTA 1680  
 AGTCTCAACC TGTGATACAA TCTTAAAATG AGGAAACAAA CTTCAACTCC TGGATTTTTT 1740  
 AGTGTATCTG ACACAGAACA CCGGGTCTAT TCTTTTTTTG TATTTTATAT TTGCTTATTT 1800  
 AAGTGTACGT TCCTTTGGTT TATAGAGAAC ACCCCCAAAT CACCTGCTTT ATTAGATGGC 1860  
 TTCCAAGTTT TCTCCTAGGT GACACTGTTG GTGCCTCAGC TGACAGGGAG CAGCTGGGTG 1920  
 CAGTGTGGCC TTTCCATGCC ACAGAGCTGT CAGAAT 1956

## (2) INFORMATION FOR SEQ ID NO. 8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 393 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: Evl Deduced Amino Acid Sequence
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO.8:

Met	Ser	Glu	Gln	Ser	Ile	Cys	Gln	Ala	Arg	Ala	Ser	Val	Met	Val	Tyr	1	5	10	15
Asp	Asp	Thr	Ser	Lys	Lys	Trp	Val	Pro	Ile	Lys	Pro	Gly	Gln	Gln	Gly	20	25	30	
Phe	Ser	Arg	Ile	Asn	Ile	Tyr	His	Asn	Thr	Ala	Ser	Ser	Thr	Phe	Arg	35	40	45	
Val	Val	Gly	Val	Lys	Leu	Gln	Asp	Gln	Gln	Val	Val	Ile	Asn	Tyr	Ser	50	55	60	
Ile	Val	Lys	Gly	Leu	Lys	Tyr	Asn	Gln	Ala	Thr	Pro	Thr	Phe	His	Gln	65	70	75	80
Trp	Arg	Asp	Ala	Arg	Gln	Val	Tyr	Gly	Leu	Asn	Phe	Ala	Ser	Lys	Glu	85	90	95	
Glu	Ala	Thr	Thr	Phe	Ser	Asn	Ala	Met	Leu	Phe	Ala	Leu	Asn	Ile	Met	100	105	110	
Asn	Ser	Gln	Glu	Gly	Gly	Pro	Ser	Thr	Gln	Arg	Gln	Val	Gln	Asn	Gly	115	120	125	
Pro	Ser	Pro	Glu	Glu	Met	Asp	Ile	Gln	Arg	Arg	Gln	Val	Met	Glu	Gln	130	135	140	
Gln	His	Arg	Gln	Glu	Ser	Leu	Glu	Arg	Arg	Ile	Ser	Ala	Thr	Gly	Pro	145	150	155	160
Ile	Leu	Pro	Pro	Gly	His	Pro	Ser	Ser	Ala	Ala	Ser	Thr	Thr	Leu	Ser	165	170	175	
Cys	Ser	Gly	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Val	Pro	Pro	Pro	Pro	Pro	180	185	190	
Thr	Gly	Ser	Thr	Pro	Pro	Pro	Pro	Pro	Leu	Pro	Ala	Gly	Gly	Ala		195	200	205	

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Gln Gly Thr Asn His Asp Glu Ser Ser Ala Ser Gly Leu Ala Ala Ala  
 210 215 220  
 Leu Ala Gly Ala Lys Leu Arg Arg Val Gln Arg Pro Glu Asp Ala Ser  
 225 230 235 240  
 Gly Gly Ser Ser Pro Ser Gly Thr Ser Lys Ser Asp Ala Asn Arg Ala  
 245 250 255  
 Ser Ser Gly Gly Gly Gly Gly Gly Leu Met Glu Glu Met Asn Lys Leu  
 260 265 270  
 Leu Ala Lys Arg Arg Lys Ala Ala Ser Gln Thr Asp Lys Pro Ala Asp  
 275 280 285  
 Arg Lys Glu Asp Glu Ser Gln Thr Glu Asp Pro Ser Thr Ser Pro Ser  
 290 295 300  
 Pro Gly Thr Arg Ala Thr Ser Gln Pro Pro Asn Ser Ser Glu Ala Gly  
 305 310 315 320  
 Arg Lys Pro Trp Glu Arg Ser Asn Ser Val Glu Lys Pro Val Ser Ser  
 325 330 335  
 Leu Leu Ser Arg Val Lys Pro Ala Gly Ser Val Asn Asp Val Gly Leu  
 340 345 350  
 Asp Ala Leu Asp Leu Asp Arg Met Lys Gln Glu Ile Leu Glu Glu Val  
 355 360 365  
 Val Arg Glu Leu His Lys Val Lys Glu Glu Ile Ile Asp Ala Ile Arg  
 370 375 380  
 Gln Glu Leu Ser Gly Ile Ser Thr Thr  
 385 390

## (2) INFORMATION FOR SEQ ID NO. 9:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 740 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO. 9:

Met Ser Glu Gln Ser Ile Cys Xaa Ala Arg Ala Xaa Val Met Val Tyr  
 1 5 10 15  
 Asp Asp Xaa Xaa Lys Lys Trp Val Pro Xaa Xaa Xaa Gly Xaa Xaa Gly  
 20 25 30  
 Phe Ser Arg Val Xaa Ile Tyr His Xaa Xaa Xaa Xaa Asn Thr Phe Arg  
 35 40 45  
 Val Val Gly Arg Lys Leu Gln Xaa Asp Xaa Gln Val Val Ile Asn Cys  
 50 55 60  
 Xaa Ile Xaa Lys Gly Leu Lys Tyr Asn Gln Ala Thr Pro Thr Phe His  
 65 70 75 80  
 Gln Trp Arg Asp Ala Arg Gln Val Tyr Gly Leu Asn Phe Xaa Ser Lys  
 85 90 95  
 Glu Asp Ala Xaa Xaa Phe Ala Xaa Ala Met Xaa Xaa Ala Leu Glu Xaa  
 100 105 110



Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Pro Xaa Xaa Xaa  
 115 120 125  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Val Xaa Asn Gly Pro Ser  
 130 135 140  
 Xaa Glu Glu Xaa Xaa Xaa Gln Xaa Arg Gln Xaa Xaa Xaa Xaa Xaa Xaa  
 145 150 155 160  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 165 170 175  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 180 185 190  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 195 200 205  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 210 215 220  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Glu  
 225 230 235 240  
 Arg Arg Xaa Ser Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 245 250 255  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 260 265 270  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 275 280 285  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 290 295 300  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 305 310 315 320  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 325 330 335  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 340 345 350  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 355 360 365  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 370 375 380  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 385 390 395 400  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Pro Pro Ala  
 405 410 415  
 Pro Xaa Xaa Xaa Pro Xaa Xaa Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 420 425 430  
 Xaa Pro Pro Pro Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Pro Pro Pro  
 435 440 445  
 Pro Pro Xaa Xaa Xaa Xaa Xaa Gly Pro Pro Pro Xaa Pro Xaa Xaa Pro  
 450 455 460

80

Pro Xaa Xaa Xaa Pro Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Xaa Pro Pro  
 465 470 475 480  
 Pro Ala Pro Pro Leu Pro Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 485 490 495  
 Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 500 505 510  
 Xaa Gly Leu Ala Ala Ala Xaa Ala Gly Ala Lys Leu Arg Lys Val Xaa  
 515 520 525  
 Xaa Xaa Glu Xaa Ala Ser Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 530 535 540  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 545 550 555 560  
 Xaa Xaa Gly Gly Xaa Gly Leu Met Glu Glu Met Xaa Xaa Xaa Leu Ala  
 565 570 575  
 Arg Arg Arg Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 580 585 590  
 Lys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Pro Xaa Xaa Xaa Xaa Xaa Xaa  
 595 600 605  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Glu Xaa Xaa Arg  
 610 615 620  
 Xaa Pro Trp Glu Xaa Xaa Asn Thr Xaa Xaa Xaa Xaa Xaa Xaa Ser Xaa Xaa  
 625 630 635 640  
 Xaa Ser Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 645 650 655  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 660 665 670  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 675 680 685  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asp Leu  
 690 695 700  
 Asp Arg Xaa Lys Gln Glu Ile Leu Xaa Glu Xaa Xaa Xaa Glu Leu Xaa  
 705 710 715 720  
 Lys Val Lys Glu Glu Ile Ile Asp Ala Ile Xaa Gln Glu Leu Xaa Xaa  
 725 730 735  
 Xaa Xaa Xaa Xaa  
 740

## (2) INFORMATION FOR SEQ ID NO. 10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 5 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO. 10:

Leu Glu Arg Glu Arg  
1 5

## (2) INFORMATION FOR SEQ ID NO. 11:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 19 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO. 11:

Leu Lys Glu Glu Leu Ile Asp Ala Ile Arg Gln Glu Leu Ser Lys Ser  
1 5 10 15  
Asn Thr Ala

## (2) INFORMATION FOR SEQ ID NO. 12:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO. 12:

Ser Glu Pro Ser Ser Phe Glu Phe Pro Pro Pro Pro Thr Asp Glu Glu  
1 5 10 15  
Leu Arg Leu Ala  
20

## (2) INFORMATION FOR SEQ ID NO. 13:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 6 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO. 13:

Gly Pro Pro Pro Pro Pro  
1 5

## (2) INFORMATION FOR SEQ ID NO. 14:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: MF
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO. 14:

AATCGCACAC TCTGTCCATA TTCC

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## (2) INFORMATION FOR SEQ ID NO.15:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: MR
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO. 15:

TGCCCAACAAC TCTGAATGTG TTG

23

## (2) INFORMATION FOR SEQ ID NO. 16:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: BPAF
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO. 16:

TCCCAGTCAC GACGTTGTAA AAC

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## (2) INFORMATION FOR SEQ ID NO. 17:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 5 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO. 17:

Phe Pro Pro Pro Pro  
1 5

WHAT IS CLAIMED IS:

We claim:

I . A screening method for detecting the presence in a test  
5 sample of a modulator of activity or expression of a *Mena* protein or  
peptide, comprising the steps of:

providing a control sample including suitable amounts of *Mena*  
protein or peptide and a *Mena* binding partner under conditions that permit  
formation of complexes between the binding partner and the *Mena* protein or  
10 peptide;

providing a test sample including a test substance and  
suitable amounts of *Mena* protein or peptide and a selected *Mena*-binding  
partner under conditions that permit formation of complexes between the  
binding partner and the *Mena* protein or peptide in the absence of the test  
15 substance;

detecting complexes of *Mena* and *Mena*-binding partner in the  
test sample and in a control sample to determine whether the test  
substance is a modulator of activity or expression of the *Mena* protein or  
peptide.

## INTERNATIONAL SEARCH REPORT

International application No.  
PCT/US97/11669

**A. CLASSIFICATION OF SUBJECT MATTER**

IPC(6) : GOIN 33/53

US CL : 435/7.2

According to International Patent Classification (IPC) or to both national classification and IPC

**B. FIELDS SEARCHED**

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/7.2; 530/350

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

APS, DIALOG (medline, dissertation abstracts, biosis, embase, derwent, life sciences, conference papers, cancerlit, CAS)

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A	BLACK, M. M., "MICROTUBULE TRANSPORT AND ASSEMBLY COOPERATE TO GENERATE THE MICROTUBULE ARRAY OF GROWING AXONS", PROG BRAIN RES, 1994, VOL. 102, PAGES 61-77, SEE ENTIRE REFERENCE.	1

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*B* earlier document published on or after the international filing date	*Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
*L* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	*A* document member of the same patent family
*O* document referring to an oral disclosure, use, exhibition or other means	
*P* document published prior to the international filing date but later than the priority date claimed	

Date of the actual completion of the international search

05 SEPTEMBER 1997

Date of mailing of the international search report

16 OCT 1997

Name and mailing address of the ISA/US  
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Washington, D.C. 20231

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